

**Gag\_AF110965\_BW\_mod**

ATGGGCGCCCGGCCAGCATCCTGGCGGGCAAGCTGGACGCCCTGGGAGGCCATCCGCC  
TGCGCCCCGGCGCAAGAAGTGCTACATGATGAAGCACCTGGTGTGGCCAGCCGAGCT  
GGAGAAGTTCGCCCTGAACCCCGCCCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATCATC  
CGCCAGCTGCACCCCGCCCTGCAGACCGGGCAGOGAGGAGCTGAAGAGCCTGTTCAACACCG  
TGGCCACCCCTGTACTGCGTGACCGAGAAGATCGAGGTGCGCAGACCCAAGGAGGCGCTGGA  
CAAGATCGAGGAGGAGCAGAACAAAGTGCCAGCAGAAGATCCAGCAGGCCAGGCCGAC  
AAGGGCAAGGTGAGCCAGAACTACCCCATCGTCAGAACCTGCAGGGCCAGATGGTGCACC  
AGGCCATCAGCCCCCGCACCGTGAACGCCCTGGTGAAGGTGATCGAGGAGAAGGCCTTCAG  
CCCCGAGGTGATCCCCATGTTACCGCCCTGAGCGAGGGGCCACCCCCCAGGACCTGAAAC  
ACGATGTTGAAACACCGTGGCGGCCACCAGGCCCATGCAGATGCTGAAGGACACCATCA  
ACGAGGAGGCCGCGAGTGGGACCGCGTGCACCCCGTGCACGCCGCCCATGCCCGG  
CCAGATGCGCGAGCCCCCGGCAGCGACATGCCGGACCACCAAGCACCCCTGCAGGAGCAG  
ATGCCCTGGATGACCAGCAACCCCCCATCCCCGTGGCGACATCTACAAGCGGTGGATCA  
TCCTGGGCCTGAAACAGATCGTGGGATGTACAGCCCCGTGAGCATCCTGGACATCAAGCA  
GGGCCCCAAGGAGCCCTCCGCGACTACGTGGACCGCTTCTCAAGACCCCTGCCGCCGAG  
CAGAGCACCCAGGAGGTGAAGAACTGGATGACCGACACCCCTGCTGGTGCAGAACGCCAAC  
CCGACTGCAAGACCATCCTGCCGCTCTGGCCCGGCCAGCCTGGAGGAGATGATGAC  
CGCCTGCCAGGGCGTGGCGGCCAGCCACAAGGCCGCGTGCCTGGCCGAGGCGATGAGC  
CAGGCCAACACCAAGCGTGAATGATGCGAGAACCTCAAGGGCCCCCGGCCATCGTCA  
AGTGCTTCAACTGCCGCAAGGAGGCCACATGCCGCAACTGCCGCCCCCCCGCAAGAA  
GGGCTGCTGGAAGTGGCGCAAGGAGGCCACCAAGATGAAGGACTGCACCGAGGCCAGGCC  
AACTTCCCTGGCAAGATCTGGCCAGCCACAAGGGCCGCCGCAACTTCCCTGCAGAGCC  
GCCCGAGCCCACCGCCCCCCCCGCCAGAGCTCCGCTTCCGAGGAGACCACCCCGGCCA  
GAAGCAGGAGGAGCAAGGACCGCGAGACCCCTGACCAGCCTGAAGAGCCTGTTGGCAACGAC  
CCCTGAGCCAGTAA

Figure 1

**Gag\_AF110967\_BW\_mod**

ATGGGCGCCCGCGCCAGCATTCTGCGCGCGAGAAGCTGGACAAGTGGAGAAGATCCGCC  
TGCAGCCCCGGCGGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGAGCT  
GGAGGGCTTCGCCCTGAACCCGGCTGCTGGAGACCGCCGAGGGCTGCAAGCAGATCATG  
AAGCAGCTGCAGCCCCCCTGCAGACCGGCACCGAGGAGCTGCGCAGCCTGTACAACACCG  
TGGCCACCCCTGTACTGCGTGCACGCCGCATCGAGGTCCGCACACCAAGGAGGCCCTGGA  
CAAGATCGAGGAGGAGCAGAACAAAGTCCCAGCAGAAGACCCAGCAGGCCAAGGAGGCCGAC  
GGCAAGGTGAGCCAGAACTACCCATCGCAGAACCTGCAGGGCCAGATGGTGCACCAGG  
CCATCAGCCCCCGCACCCCTGAACGCCCTGGTGAAGGTGATCGAGGAGAAGGCGCTTCAGGCC  
CGAGGTGATCCCCATGTTCACCGCCCTGAGCGAGGGGCCACCCCCCAGGACCTGAACACG  
ATGTTGAACACCGTGGCGGCCACCGCCGCATGCAGATGCTGAAGGACACCATCAACG  
AGGAGGCCGCCAGTGGGACCGCCTGCACCCCGTGCAGGCCGGCCCTGGCCCCCGGCCA  
GATGCGCGACCCCCCGGCCAGCGACATGCCGGGCCACCAAGCACCCCTGCAGGAGCAGATC  
GCCTGGATGACCAGCAACCCCCCGTGCCTGGCGACATCTACAAGCGGTGGATCATCC  
TGGGCTGAACAAGATCGTGGGATGTACAGCCCGTGAGCATTGGACATCCGCCAGGG  
CCCCAAGGAGGCCCTCCGCGACTACGTGGACCGCTTCTTCAAGACCCTGCGCGCCAGCAG  
GCCACCCAGGACGTGAAGAACTGGATGACCGAGACCCCTGCTGGTGAGAACGCCAACCCCG  
ACTGCAAGACCATCCTGCGCGCTCTCGGCCCCGGGCCACCCCTGGAGGAGATGATGACCGC  
CTGCCAGGGCGTGGCGGCCACAGGCCCGTGCCTGGCGAGGCGATGAGCCAG  
GCCAACAGCGTGAACATCATGATGCAGAAGAGCAACTTCAAGGGCCCCGGCGAACGTCA  
AGTGCTTCAACTGCGGCAAGGAGGGCCACATGCCAAGAACTGCCGCCCGCAAGAA  
GGGCTGCTGGAAGTGCAGGCAAGGAGGGCCACAGATGAAGGACTGCACCGAGGCCAGGCC  
AACTTCTGGCAAGATCTGGCCAGCCACAAGGGCCGCCGGCAACTTCTGCAGAACCC  
GCAGCGAGCCCCGGCCACCGTGCCTGGGCCACCGCCCCCGGCCAGAGCTTCCGCTTCGA  
GGAGACCAACCCCCGGCCCAAGCAGGAGGCCAAGGAGCCGAGGCCCTACCGCGAGGCCCTG  
ACCGCCCTGCGCAGCCTGTTGGCAGGGCCCCCTGAGCCAGTAA

Figure 2

**Fig. 3**

**Env\_AF110968\_C\_BW\_opt**

--> **signal peptide (1-81)**  
ATGC CGT GAT GGG C AT CCT G AAG A ACT ACC A CG A GT G G T G G AT G T G G G C AT C C T G G G C T T C T G G AT G C T G AT C A  
\\--> **gp120/140/160 (82)**  
TCAG C AG C G T G G T G G G C A A C C T G T G G G T G A C C G T G A C T A C G G C T G C C C G T G T G G A A G G A G G C C A A G A C C A C C T  
GTT C T G C A C C A G C G A C G C C A A G G C C T A C G A G A C C G A G G T G C A C A A C G T G T G G G C C A C C C A C G C C T G C G T G C C C A C C  
G A C C C C A A C C C C A G G A G A T C G T G C T G G A G A A C G T G A C C G A G A A C T T C A A C A T G T G G A A G A A C G A C A T G G T G G A C C  
A G A T G C A C G A G G A C A T C A T C A G C C T G T G G G A C C A G A G C C T G A A G C C C T G C G T G A A G C T G A C C C C C T G T G C G T G A C  
C C T G A A G T G C C G C A A C G T G A A C G C C A C C A A C A C A T C A A C A G C A T G A T C G A C A A C A G C A A C A A G G G C G A G A T G A A G  
A A C T G C A G C T T C A A C G T G A C C A C C G A G C T G C G C G A C C G C A A G C A G G A G G T G C A C G C C T G T T C T A C C G C T G G A C G  
T G G T G C C C T G C A G G G C A A C A C A G C A A C G A G T A C C G C C T G A C T G C A A C A C C A G C G C C A T C A C C C A G G C C T G  
C C C C A A G G T G A G C T T C G A C C C C A T C C C C A T C C A C T A C T G C A C C C C C G C C G G C T A C G C C A T C C T G A A G T G C A A C A A C  
C A G A C C T T C A A C G G C A C C G G C C C C T G C A A C A C A G C T G A G C A G C G T G C A G T G C G C C C A C G G C A T C A G C C C G T G G T G A  
G C A C C C A G C T G C T G C A A C G G C A G C C T G G C A A G G G C G A G A T C A T C A C C G C A G C G A G A A C C T G G C C A A C A A C G  
C A A G A T C A T C A T C G T G C A G C T G A A C A A G C C C G T G A A G A T C G T G C G T G C G C C C A A C A A C A A C A C C C G C A A G A G C  
G T G C G C A T C G G C C C C G G C C A G A C C T T C A C G C C A C C G G C G A G A T C A T C G G C G A C A T C C G C C A G G C C T A C T G C A T C A  
T C A A C A A G A C C G A G T G G A A C A G C A C C C T G C A G G G C G T G A G G A A G A A G C T G G A G G A G C A C T T C A G C A A G A A G G C C A T  
C A A G T T C G A G C C C A G C A G C G G C G G C G A C C T G G A G A T C A C C A C C C A C A G G C T T C A A C T G C C G C G G C G A G T T C T T C A C  
T G C G A C A C C A G C C A G C T G T C A A C A G C A C C T A C A G C C C C A G C T T C A A C G G C A C C G A G A A C A A G C T G A A C G G C A C C A  
T C A C C A T C A C C T G C C G C A T C A A G C A G A T C A T C A A C A T G T G G C A G A A G G T G G G C C G C C A T G T A C G C C C C C C C A T  
C G C C G G C A A C C T G A C C T G C G A G A G C A A C A T C A C C G G C C T G C T G C G A C C C G G C A C G G C G G C A A G A C C G G C C C C A A C  
G A C A C C G A G A T C T T C G C C C C G G C G G C G G C G A C A T G C G C G A C A A C T G G G C G A C A C G A G G C T G T A C A A G T A C A A G G T G G  
T G G A G A T C A A G C C C T G G G C G T G G G C C C C A C C G A G G C C A A G C G C C G C G T G G G A G G C G G A A G C G C G C C G T G G G  
C A T C G G C G C C G T G T C C T G G G C T T C C T G G G C G C C G C G C A G C A C C A T G G G C G C C G C A G C A T C A C C C T G A C C G T G  
C A G G C C C C C T G C T G C G A G C G G C A T C G T G C A G C A G A A C A A C C T G C T G C G C C C A T C G A G G G C C A G C A G C A C C  
T G C T G C A G C T G A C C G T G T G G G C A T C A A G C A G C T G C A G A C C C G C A T C C T G G C C G T G G G C G C T A C C T G A A G G A C C A  
G C A G C T G C T G G G C A T C T G G G C T G C A G C G G C A A G C T G A T C T G C A C C A C C G C G T G C C C T G G A A C A G C A G C T G G G A G C  
A A C C G C A G C C A C G C A G G A G A T C T G G G C A A C A T G A C C T G G G A T G C A G T G G G A C C G C G A G A T C A A C A A C T A C A C C G A C A  
C C A T C A C C G C C T G C T G G A G G A G A G C C A G A A C C A G C A G G G A A G A A C G C A G A G A A G G A C C T G C T G G C C C T G G A C A G C T G  
gp140 (2025) <--\\  
G C A G A A C C T G T G G A A C T G G T T C A G C A T C A C C A A C T G G C T G G T A C A T C A A G A T C T T C A T C A T G A T C G T G G G C G G C  
C T G A T C G G C C T G C G C A T C A T C T C G C C G T G C T G A G C A T C G T G A A C C G C G T G C G C C A G G G C T A C A G C C C C C T G C C C T  
T C C A G A C C C T G A C C C C C A A C C C C G C G A G C C C G A C C G C C T G G G C C G C A T C G A G G A G G G C G G G C A G C A G G A C C G  
C G G C C G C A G C A T C C G C C T G G T G A G C G G C T T C C T G G G C C T G G C C G A C C T G C G C A G C C T G T G C C T G T C A G C  
T A C C A C C G C C T G C G C G A C T T C A T C C T G A T C G C C G C C C G C G T G C T G G A G G C T G C T G G G C C A G C G C G G C T G G G A G G C C C  
T G A A G T A C C T G G G C A G C C T G G T G C A G T A C T G G G G C C T G G G A G G C T G A A G A A G A G G C G C C A T C A G C C T G T G G A C A C C A T  
C G C C A T C C G C C T G G G C C A G G G C A C C G C A C C G C A T C A G G T T C A T C C A G C G C A T C T G C C G C G C C A T C C G C A A C A T C  
CCCC G C C G C A T C C G C C A G G G C T T C G A G G C C G C C C T G C A G T A A A

Fig. 4

### Env\_AF110975\_C\_BW\_opt

--> signal peptide (1-72)  
ATGCGCTGCGCGCATCCTGCGCAGCTGGCAGCAGTGGGATCTGGGCATCCTGGCTTCTGGATCTGCAGCG  
gp120/140/160 (72)  
GCCTGGCAACCTGGGTGACCGTGTACGACGGCGTGCCTGTGGCGAGGCCAGCACCAACCTGTTCTGCGC  
CAGCGACGCCAAGGCCAACGAGGAGGTGCACAACGTCGGGCCACCCACGCCCTGCCTGCCACCAGACCCCAAC  
CCCCAGGAGATCGAGCTGGACAACGTCACCGAGAACCTCAACATGTGGAAGAACGACATGGTGGACCAGATGCAG  
AGGACATCATCAGCTGTGGGACAGAGCCTGAAGCCCCCGTGAAGCTGACCCCCCTGTGCCTGACCTGAAGTG  
CACCAACTACAGCACCAACTACAGCAACACCATGAACGCCACCAGCTACAACAACACCACCGAGGAGATCAAG  
AACTGCACCTCAACATGACCACCGAGCTGCGCACAAGAACGAGCAGCAGGTGTACGCCCTGTTCTACAAGCTGGACA  
TCGTGCCCTGAACAGCAACAGCAGCGAGTACCGCCTGATCAACTGCAACACCAGCGCCATCACCCAGGCCCTGCC  
CAAGGTGAGCTCGACCCCCATCCCCATCCACTACTGCGCCCCCGCCGCTACGCCATCCTGAAGTGCAAGAACAC  
ACCAGCAACGGCACCGGCCCCCTGCCAGAACGTGAGCACCGTGCAGTGACCCACGGCATCAAGCCGTGGTGAGCA  
CCCCCCTGCTGCTGAACGGCAGCCTGGCGAGGGCGGGAGATCATCATCCGCAAGAACCTGAGCAACAACGC  
CTACACCATCATCGTGCACCTGAACGACAGCGTGGAGATCGTGTGCACCCGCCAACACAACACCCGCAAGGGC  
ATCCGCATCGGCCCCGGCAGACCTCTACGCCACCGAGAACATCATCGCGACATCCGCCAGGCCACTGCAACA  
TCAGCGCCGGCAGTGGAAACAAGGCCGTGCAAGCGCTGAGCGCAAGCTGCGCGAGCACTCCCCAACAAAGACCAT  
CGAGTTCCAGCCCCAGCAGCGGGGCGACCTGGAGATCACCAACCCACAGCTCAACTGCCGCGGAGTTCTTCTAC  
TGCAACACCAAGCTGTTAACAGCAGCTAACAGGCCACCGAGCTACCGCGGACCCAGAACAGCAGCATCA  
TCACCCCTGCCCTGCCCATCAAGCAGATCATCGACATGTGGCAGAAGGTGGCCGCGCCATCTACGCCCTGCC  
CGAGGGCAACATCACCTGCAGCAGCAGCATCACCGCCTGCTGCTGGCCCGCGACGGCGGCCCTGGACAACATCACC  
ACCGAGATCTTCCGCCCGACATGAAGGACAACGGCGCAACGAGCTGTACAAGTACAAGTGGTGG  
gp120 (1509) <--\--> (1510) gp11  
AGATCAAGCCCCCTGGCGTGGCCCCACCGAGGCCAAGCGCCGCGTGGTGGAGCGCGAGAACGCGCCGCGTGGCGAT  
CGGCGCCGTGATCTCGGCTTCTGGCGCCGGCAGCAACATGGCGCCGCCAGCATCACCCCTGACCGCCAG  
GCCCGCCAGCTGCTGAGCGCATCGTGCAGCAGAGCAACCTGCTGCGCGCCATCGAGGCCAGCAGCACATGC  
TGCAGCTGACCGTGTGGGCATCAAGCAGCTGCAGGCCCGCGTGGCCATCGAGCGCTACCTGAAGGACCAGCA  
GCTGCTGGCATCTGGGCTGCAAGCGCAAGCTGATCTGACCAACCCGTCGCCCTGGAACAGCAGCTGGAGCAAC  
AAGACCCAGGGCGAGATCTGGGAGAACATGACCTGGATGCAGTGGACAAGGAGATCAGCAACTACACCGCAGCATCA  
TCTACCGCCTGCTGGAGGAGAGCCAGAACCGAGCAGGAGCAGAACGAGAAGGACCTGCTGGCCCTGGACAGCGCAA  
gp140 (2022) <--\-->  
CAACCTGTGGAGCTGGTCAACATCAGCAACTGGCTGTGGTACATCAAGATCTTCATCATGATCGTGGCCGCGCTG  
ATCGGCCCTGCCCATCATCTGCCGTGCTGAGCATCGTGAACCGCGTGCCTGCCAGGGCTACAGCCCCCTGAGCTTCC  
AGACCCCTGACCCCCAACCCCCCGCCGCTGGACCGCCTGGCCCTGGACGACCTGCGCAGCCTGTGCCTGTTCAAGCTAC  
CCGCAGCATCCGCCCTGGTGCAGGGCTTCCCTGGCCCTGGCAGACCTGCGCAGCCTGTGCCTGTTCAAGCTAC  
CACCGCCTGCCGACCTGATCTGGTACCGCCCGCGTGGTGGAGCTGCTGGCCCGCAGCAGCCCCCGCGGCCCTGC  
AGCGCGCTGGAGGCCCTGAAGTACCTGGCAGCCTGGTCAAGTACTGGGCTGGAGCTGAAGAACAGCGCCAC  
CAGCCTGCTGGACAGCATGCCATGCCGTGGCCAGGGCACCGACCGCATCGAGGTGATCCAGCGCATCTAC  
gp160, gp41 (2565) <--\-->  
CGCGCCTCTGCAACATCCCCCGCCGCGTGCAGGCCAGGGCTTCGAGGCCGCCCTGCAGTAA

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ATGGGGCGCCCGCGCCAGCATCCTGCGCGGCCAGCTGGACGCCCTGGGAGCCATCCGCCCTGGGCCCCGG  
CGGCAAGAAGTGTACATGATGAAGCACCTGGTGTGGGCCAGCCGAGCTGGAGAAGTTCGCCCTGAACC  
CGGGCCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATCATCCGCCAGCTGCACCCGCCCTGCAGACCGGC  
AGCGAGGAGCTGAAGAGCCTGTTCAACACCGTGGCCACCCCTGTACTGCGTGCACGAGAAGATCGAGGT[G]  
CGACACCAACGGAGGCCCTGGACAAGATCGAGGAGGAGCAGAACAAAGTGCACGAGAAGATCCAGCAGGCC  
AGGCCGCCACAAGGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATGGTGCAC  
CAGGCCATCAGCCCCCGCACCCCTGAACGCCCTGGTGAAGGTGATCGAGGAGAAGGCCCTCAGCCCCGAGGT  
GATCCCCATGTTACCGCCCTGAGCGAGGGGCCACCCCCCAGGACCTGAACACCATGCTGAACACCGTGG[G]  
GGGGCCACCAAGGCCATGCAGATGCTGAAGGACACCATCAACGAGGAGGCCGAGTGGGACCGCGTG  
CACCCCGTGCACGCCGCCCATGCCCGGCCAGATGCGCAGGCCCGGGCAGCGACATGCCGCCAC  
CACCAAGCACCCCTGCAGGAGCAGATGCCCTGGATGACCAGCAACCCCCCATCCCCGTGGCGACATCTACA  
AGCC[G]CTGGATCATCCTGGCCTGAACAAGATCGTGC[G]ATGTACAGCCCGTGCAGAACCTGCACATCAAG  
CAGGGCCCCAAGGAGCCCTCCCGACTACGTGGACCGCCTTCAAGACCCCTGCCGCCAGCAGAGCAC  
CCAGGAGGTGAAGAACTGGATGACCGACACCCCTGCTGGTGCAGAACGCCAACCCGACTGCAAGACCATCC  
TGCGCGCCCTGGCCCCGGGCCAGCCTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGGCCCCAGC  
CAAAAGGCCCGCTGGCCAGGCCATGAGCCAGGCCAACACCGCGTATGAGAACAGCAACTTCTGGGCGGG  
CAAGGGCCCCCGCCGCAACTCGT[G]AAAGTGCCTCAACTGCCAGGAGGCCACATGCCCGCAACTGCCCG  
CCCCCGCAAGAAGGGCTGCTGGAAAGTGCAGGCCAGGAGGCCACCAAGATGAAGGACTGCACCCGAGGCCAG  
GCCAACTTCTGGCAAGATCTGCCAGCCACAAGGGCCGCCACTTCTGCAGAGGCCGCCAG  
GCCCAACCGCCCCCCCCCGAGAGCTTCCGCTCGAGGAGGCCACCCCGGCCAGAACAGGAGAGCAAGG  
ACCGCGAGACCCCTGACCGCCTGAAGAGCCTGTTGGCAACGACCCCTGAGCCAGTAA

Figure 5

**Gag\_AF110967\_BW\_opt**  
ATGGGCGCCCGCGCCAGCATCTGGCGGCGAGAAGCTGGACAAGTGGAGAAGATCCGCTGCGCCCCGG  
CGGCAAGRAGCACTACATGCTGAGCACCTGGTGTGGGCCAGCCGGAGCTGGAGGGGTTCCGCCCCCTGAACC  
CCGGCCTGCTGGAGACCGCCGAGGGCTGCAAGCAGATCATGAAGCAGCTGCAGCCCGCCCTGCAGACCGGC  
ACCGAGGAGCTGCGAAGCCCTGTAACACACCGTGGCCACCCCTGTAAGTGGCTGCACGCCGGCATCGAGGTC  
CGACACCAAGGAGGCCCTGGACAAGATCGAGGAGGAGCACACAGACAGCAGCAGAAGACCCAGCAGGCCA  
AGGAGGCCGACGCCAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCAGATGGTGCACCAAG  
GCCATCAGCCCCCGCACCTGAACGCCCTGGTGAAGGTGATCGAGGAGAAGGCCCTCAGCCCCGAGGTGAT  
CCCCATGTTAACCGCCCTGAGCGAGGGGCCACCCCCCAGGACCTGAAACATGTCGACACCGTGGCTG  
GCCACCAGGCCATGCAAGATGCTGAAGGACACCATAACGAGGAGGCCGAGTGGACCGCCTGCAC  
CCCGTGCAGGCCGGCCCCGTGGCCCCCGCCAGATGCGCGACCCCCCGGGCAGCAGACATGCCGGGCCAC  
CAGCACCCCTGCAGGAGCAGATGCCCTGGATGACCAAGCAACCCCCCGTGCCCCGTGGCGACATCTACAAGC  
GCTGGATCATCCTGGCCTGAACAAGATCGTGCCTGACAGCAGCCCTGGTGCAGAACCTGCGACATCCGCCAG  
GGCCCCAAGGAGGCCCTCCGCACTACGTGGACCGCTTCAAGACCTGCGCCGAGCAGGCCACCCA  
GGACGTGAAAGAACTGGATGACCGAGACCCCTGCTGGTGCAGAACGCCAACCCGACTGCAAGACCATCCTGC  
GGCGCTGGCCCCGGCGCCACCCCTGGAGGAGATGATGACCGCTGCCAGGGCGTGGCGGCCAC  
AAGGCCCGTGTGGCGAGGCGATGAGCCAGGCCAACAGCGTGAACATCATGATGCAAGAGCAACTT  
CAAGGGCCCCCGCAACGTCAGTGCTCAACTGCGCAAGGAGGGCCACATGCCAAGAACTGCCGCG  
CCCCCGCAAGAAGGGCTGCTGGAAAGTGCAGGAGGCCACCAAGGACTGCAACCGAGCGCCAG  
GCCAACTTCTGGCAAGATCTGGCCAGCCACAAGGGCGCCGGCAACTTCTGCAGAACCGCAGCGA  
GCCCGCCGCCACCGTGCCTACCGGCCGGCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGCC  
CCAAGCAGGAGGCCAAGGACCGCGAGCCCTACCGCGAGCCCTGACCGCCCTGCGCAGGCCCTGTCGGCAGC  
GGCCCCCTGAGCCAGCTAA

Figure 6

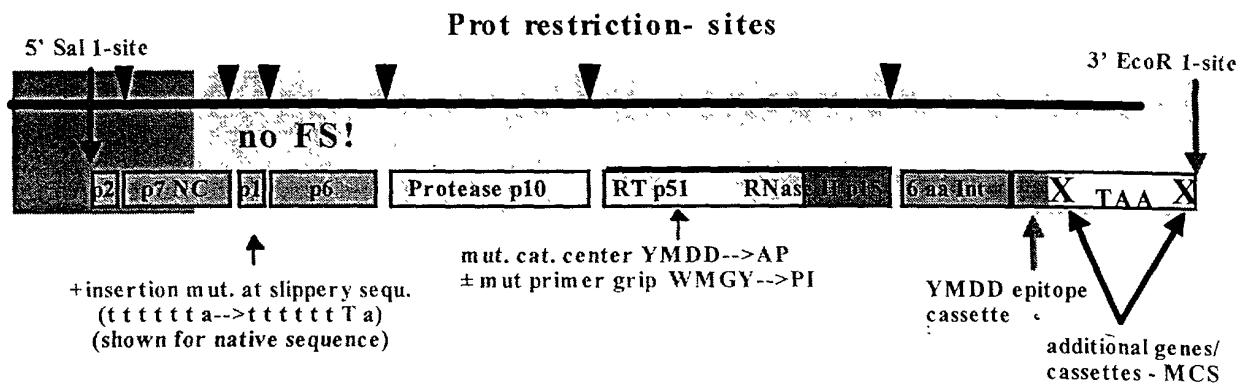


FIGURE 7

PR975(+) (SEQ ID NO:30)

GTGACGCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGGCCAACATCCTGAT  
GCAGCGCAGCAACTCAAGGGCCCAAGCGCATCATCAAGTGCTTCAACTGCGGAA  
GGAGGGCCACATCGCCCGCACTGCCGCCCGCAAGAAGGGCTGCTGGAAGT  
GCGGCAAGGAGGGCCACCAAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCTC  
CGCGAGGACCTGGCCTTCCCCCAGGGCAAGGCCCGAGTCCCCAGCGAGCAGAA  
CCGCGCCAACAGCCCCACCAAGCCCGAGCTGCAGGTGCGCCGACAACCCCGCA  
GCGAGGCCGGCGCCAGCGCCAGGGCACCCCTGAACCTCCCCAGATCACCCGTGGC  
AGCGCCCCCTGGTGAAGCATCAAGGTGGGCGGCCAGATCAAGGAGGCCCTGCTGGAC  
ACCGGCCCGACGACACCGTGTGGAGGAGATGAGCCTGCCCGCAAGTGGAAAGCC  
CAAGATGATCGGCCGCATCGCGGCTTCATCAAGGTGCGCCAGTACGACCAGATCCT  
GATCGAGATCTCGGCAAGAAGGCCATCGGCCACCGTGTGATCGGCCCAACCCCGT  
GAACATCATCGGCCCAACATGCTGACCCAGCTGGGCTGACCCCTGAACCTCCCCAT  
CAGCCCCATCGAGACCGTGGCCGTGAAGCTGAAGGCCGATGGACGGCCCCAAGG  
TGAAGCAGTGGCCCTGACCGAGGAGAAGATCAAGGCCCTGACGCCATCTGCGAG  
GAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCGAGAACCCCTACAACAC  
CCCCGTGTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACT  
TCCCGAGCTGAACAAGCGCACCCAGGACTCTGGGAGGTGCAGCTGGCATCCCC  
ACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGAACCGTGTGGACGTGGCGACGCC  
TACTTCAGCGTCCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTTCACCATCCCC  
AGCATCAACAAACGAGACCCCCGGCATCCGCTACCAAGTACAACGTGCTGCCAGGGC  
TGGAAAGGGCAGCCCCAGCATCTTCAGAGCAGCATGACCAAGATCCTGGAGGCCCTC  
CGCGCCCGCAACCCCGAGATCGTGTACCTACCAAGTACATGGACGACCTGTACGTGGC  
AGCGACCTGGAGATCGGCCAGCACCGCCAAGATCGAGGAGCTGCGCAAGCACCT  
GCTGCGTGGGGCTTCACCACCCCGACAAGAAGCACCAGAAGGAGCCCCCTTCCT  
GTGGATGGCTACGAGCTGCACCCGACAAGTGGACCGTGCAGCCATCGAGCTGCC  
CGAGAAGGAGAGCTGGACCGTGAACGACATCCAGAAGCTGGTGGCAAGCTGAAC  
GGGCCAGCCAGATCTACCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGCGCG  
GCGCCAAGGCCCTGACCGACATCGTCCCCGTGACCGAGGAGGCCAGTGGAGCTG  
GCCGAGAACCGCGAGATCTGCGCAGCCGTGACGGCGTGTACTACGACCCAG  
CAAGGACCTGGTGGCGAGATCCAGAAGCAGGGCACGACCAAGTGGACCTACCA  
TCTACCAGGAGGCCCTCAAGAACCTGAAGGACCGCAAGTACGCCAAGATGCGCACC  
GCCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGAGAAGATCGCCATGGA  
GAGCATCGTGTACGGGCAAGACCCCCAAGTCCGCTGCCATCCAGAAGGAGAC  
CTGGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGAGTT  
CGTGAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAAGCTGGAGAAGGAGCCATCAT  
CGGCGCCGAGACCTTCTACGTGGACGGCCGCCAACCGCGAGACCAAGATCGGCA  
AGGCCGGTACGTGACCGACGCCAGTACGCCCTGGCATCATCCAGGCCAGCC  
ACCAACCAGAAGACCGAGCTGCAGGCCATCCAGCTGCCCTGCAGGACAGCGGAG  
CGAGGTGAACATCGTACCGACAGCCAGTACGCCCTGGCATCATCCAGGCCAGCC  
CGACAAGAGCGAGAGCGAGCTGGTAACCAGATCATCGAGCAGCTGATCAAGAAGG  
AGAAGGTGTACCTGAGCTGGGTGCCGCCACAAGGGCATGGCGCAACGGAGCAG  
ATCGACAAGCTGGTGAAGCAAGGGCATCCGCAAGGTGCTGTTCTGGACGGCATCGAT  
GGCGGCATCGTGTACCAAGTACATGGACGACCTGTACGTGGCAGCGGCCG  
AGGATCGATTAAAGCTCCGGGGTAGCACCGGTGAATT

FIGURE 8

**PR975YM (SEQ ID NO:31)**

GTCGACGCCACCATGGCCGAGGCCATGAGCCAGGCCACCAGGCCAACATCCTGAT  
GCAGCGCAGCAACTCAAGGGCCCAAGCGCATCATCAAGTGCTCAACTGCCGCAA  
GGAGGGCCACATGCCCGCAACTGCCGCCCGCAAGAAGGGCTGCTGGAAGT  
GCGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGGCCAGGCCACTCTTC  
CGCGAGGACCTGCCCTCCCCCAGGGCAAGGCCGCGAGTCCCCAGCGAGCAGAA  
CCCGCACAACAGCCCCACCAGCCCGAGCTCAGGTGCGCCGACAACCCCCGCA  
GCGAGGCCGGCGCCGAGGCCAGGGCACCCCTGAACCTCCCCAGATCACCTGTGGC  
AGCGCCCCCTGGTGAGCATCAAGGTGGCCGAGATCAAGGAGGCCCTGCTGGAC  
ACCGGCCGACGACACCGTGTGGAGGAAGATGAGCCTGCCGCAAGTGGAAAGCC  
CAAGATGATCGCGGCATCGCGGCTTCATCAAGGTGCGCCAGTACGACCAGATCCT  
GATCGAGATCTGCCGCAAGAAGGCCATCGGCCACCGTGTGATCGGCCACCCCGT  
GAACATCATCGGCCGCAACATGCTGACCCAGCTGGCTGCACCCCTGAACCTCCCCAT  
CAGCCCCATCGAGACCGTGTGGAGCTGAAGCTGAAGGCCGATGGACGGCCCCAAGG  
TGAAGCAGTGGCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCGAG  
GAGATGGAGAAGGAGGGCAAGATACCAAGATGCCCGAGAACCCCTACAACAC  
CCCCGTGTTGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACT  
TCCCGAGCTGAACAAGCGCACCCAGGACTCTGGGAGGTGCAGCTGGCATCCCCC  
ACCCCGCCGGCCTGAAGAAGAAGAAGAGCGTGCACCGTGTGGACGTGGCGACGCC  
TACTTCAGCGTGCCCTGGACGAGGACTTCGCAAGTACACCGCCTTCACCATCCCC  
AGCATCAACAACGAGACCCCCGGCATCCGCTACCAAGTACAACGTGTGCCCGAGGGC  
TGGAAAGGGCAGCCCCAGCATCTTCAGAGCAGCATGACCAAGATCTGGAGGCCCTTC  
CGCGCCCGCAACCCCGAGATCGTGTACCTACCGCCCCCTGTACGTGGCGACGCC  
CTGGAGATCGGCCAGCACCGCGCCAAGATCGAGGAGCTGCCAAGCACCTGCTGCG  
CTGGGCTTCACCAACCCCCGACAAGAACGACCAAGAACGGAGGCCCTTCCTGTTGGAT  
GGGCTACGAGCTGCACCCGACAAGTGGACCGTGCAGCCATCGAGCTGCCGAGA  
AGGAGAGCTGGACCGTGAACGACATCCAGAACGACTGGTGGCAAGCTGAACGGGCC  
AGCCAGATCTACCCCGCATCAAGGTGCGCCAGCTGTGCAAGCTGCTGCCGCGGCC  
AAGGCCCTGACCGACATCGTGCCCTGACCGAGGAGGCCAGCTGGAGCTGCCGA  
GAACCGCGAGATCCTGCCGAGGCCCTGACCGACCGTGTACTACGACCCAGCAAGG  
ACCTGGTGGCCGAGATCCAGAACGAGGGCACGACCAAGTGTGACCTACCAAGATCTAC  
CAGGAGCCCTCAAGAACCTGAAGACCGCAAGTACGCCAAGATGCCACCGCCA  
CACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAACGATGCCATGGAGAGCA  
TCGTGATCTGGGCAAGACCCCCAAGTCCGCTGCCATCCAGAACGGAGACCTGGG  
AGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCCCAGTGGAGTTCTGTA  
ACACCCCCCCCCCTGGTGAAGCTGTGGTACCGAGCTGGAGAACGGAGCCATCATCGCG  
CCGAGACCTTCTACGTGGACGGCGCCAACCGCGAGACCAAGATCGCAAGGCC  
GGCTACGTGACCGACCGGGGCCAGAACGATCGTGTGGCTGACCGAGACCAAGGCC  
CCAGAACCGAGCTGCAGGCCATCCAGCTGGCCCTGACGGACAGCGGAGCGAGG  
TGAACATCGTACCGACAGCCAGTACGCCCTGGGATCATCCAGGCCAGCCGACA  
AGAGCGAGAGCGAGCTGGTGAACCAAGATCATCGAGCAGCTGATCAAGAACGGAGAAG  
GTGTACCTGAGCTGGGTGCCGCCACAAGGGCATCGCGCAACGAGCAGATCGA  
CAAGCTGGTGAGCAAGGGCATCCGCAAGGTGCTGTTCTGGACGGCATCGATGGCG  
GCATCGTATCTACCAAGTACATGGACGACCTGTACGTGGCAGCGGCCCTAGGA  
TCGATTAAGCTCCGGGCTAGCACCGGTGAATT

**FIGURE 9**

PR975YMWM (SEQ ID NO:32)

GTGCACGCCACCATGGCGAGGCCATGCCAGGCCACCAGGCCAACATCCTGAT  
GCAGCGCAGCAACTCAAGGGCCCAAGCGCATCATCAAGTGCTCACTGCGGCAA  
GGAGGGCCACATGCCGCAACTGCCGCCCGCAAGAAGGGCTGCTGGAAGT  
GCGCAAGGAGGGCACCAGATGAAGGACTGCCAGGCCAGGCCAACTCTC  
CGCAGGACCTGGCTCCCCAGGGCAAGGCCCGAGTCCCCAGCGAGCAGAA  
CCGCACACAGCCCCACCAGCGCGAGCTGCCAGGTGCGCGGCGACAACCCCGCA  
GCGAGGCCGGCGGCCAGCGCCAGGGCACCCCTGAACCTCCCCAGATCACCTGTGGC  
AGCGCCCCCTGGTGAGCATCAAGGTGGCGGCCAGATCAAGGAGGCCCTGCTGGAC-  
ACCGCGCCGACGACACCGTGCTGGAGGAGATGAGCCTGCCGGCAAGTGGAAAGCC  
CAAGATGATCGGCGGACATCGGCGGCTCATCAAGGTGCCAGTACGACCAGATCCT  
GATCGAGATCTGCCGCAAGAAGGCCATGCCACCGTGTGATGCCACCCACCCCGT  
GAACATCATCGGCCGCAACATGCTGACCCAGCTGGCTGCCACCTGAACCTCCCCAT  
CAGCCCCATCGAGACCGTGCCCGTAAGCTGAAGGCCAGTGGACGGCCCCAAGG  
TGAAGCAGTGGCCCCCTGACCGAGGAGAAGATCAAGGCCCTGACGCCATCGAG  
GAGATGGAGAAGGAGGGCAAGATACCAAGATCGGCCCGAGAACCCCTACAACAC  
CCCCGTGTTGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACT  
TCCCGAGCTGAACAAAGCGCACCCAGGACTTCTGGAGGTGCAGCTGGCATCCCC  
ACCCCGCCGGCTGAAGAAGAAGAGCGTGCACCGTGTGGACGTGGCGACGCC  
TACCTCAGCGTCCCCCTGGACGAGGACTTCCGCAAGTACACCGCCTCACCATCCCC  
AGCATCAACAAACGAGACCCCCGGCATCCGCTACCAAGTACAACGTGCTGCCAGGGC  
TGGAAAGGGCAGCCCCAGCATCTCCAGAGCGACATGCCAACAGATCTGGAGGCCCTC  
CGGCCCGCAACCCCGAGATCGTGTACCTACAGGCCCTGTACGTGGCAGCGAC  
CTGGAGATCGGCCAGCACCGGCCAAGATCGAGGAGCTGCCAAGCACCTGCTGCG  
CTGGGGCTTCAACCACCCCGACAAGAACGACCAAGAACGGAGCCCCCTTCCCTGCCAT  
CGAGCTGCACCCCGACAAGTGGACCGTGCAGCCATCGAGCTGCCAGAACGGAGA  
GCTGGACCGTGAACGACATCCAGAACGACTGGTGGCAAGCTGAACCTGGCCAGGCCAG  
ATCTACCCCGGCATCAAGGTGCCAGCTGTGCAAGCTGCGCGGCCAAGGCC  
CTGACCGACATCGTCCCCGTACCGAGGAGGCCAGCTGGAGCTGGCGAGAACCG  
CGAGATCTCGCGCAGGCCGTGCACGGCGTGTACTACGACCCAGCAAGGACCTGGT  
GGCCGAGATCCAGAACGAGGGCCACGACCAAGTGGACCTACCAAGATCTACCAAGGAGC  
CTTCAAGAACCTGAAGAACCGGCAAGTACGCCAACGATGCCACCGCCCACACCAAC  
GACGTGAAGCAGCTGACCGAGGCCGTGCAGAACGATGCCATGGAGAGCATCGTGT  
CTGGGGCAAGACCCCCAAGTCCGCGCTGCCATCCAGAACGGAGACCTGGAGACCT  
GGTGGACCGACTACTGGCAGGCCACCTGGATCCCCGAGTGGAGGTTCTGTGAACACCC  
CCCCCTGGTGAAGCTGTTACCAAGCTGGAGAACGGAGGCCATCATGGCGGCCAG  
ACCTCTACGTGGACGGCGGCCAACCGCAGAACGATGCCAAGGCCGGCTA  
CGTGACCGACGGGGCGGCAGAACGATCGTGCACCGAGAACCAACCAAG  
AGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGCAGCGAGGTGAAC  
ATCGTACCGACAGCCAGTACGCCCTGGGCATCATCCAGGCCAGGCCACAAGAG  
CGAGAGCGAGCTGGTGAACCAAGCAGATCATCGAGCAGCTGATCAAGAACGGAGAACGGTGT  
ACCTGAGCTGGGTGCCGCCACAAGGGCATGGCGAACGAGCAGATCGACAAG  
CTGGTGAAGCAAGGGATCCGCAAGGTGCTGTTCTGGACGGCATCGATGGCGGCATC  
GTGATCTACCAAGTACATGGACGACCTGTACGTGGCAGCGGGCGGCCCTAGGATCGAT  
TAAAAGCTCCGGGGTAGCACCGGTGAATT

**FIGURE 10**

8\_5\_ZA (SEQ ID NO:33)

1 TGGAAGGGTT AATTACTCC AAGAAAAGGC AAGAAATCCT TGATTGTGG GTCTATCACA  
61 CACAAGGCTT CTTCCCTGAT TGGCAAAACT ACACACCGGG GCCAGGGGTC AGATATCCAC  
121 TGACCTTTGG ATGGTGTAC AAGCTAGTGC CAGTTGACCC AGGGGAGGTG GAAGAGGCCA  
181 ACGGAGGAGA AGACAACGTG TTGCTACACC CTATGAGCCA ACATGGAGCA GAGGATGAAG  
241 ATAGAGAAGT ATTAAAGTGG AAGTTGACA GCCTCCTAGC ACCCAGACAC ATGGCCCGCG  
301 AGCTACATCC GGAGTATTAC AAAGACTGCT GACACAGAAG GGACTTCCC CCTGGGACTT  
361 TCCACTGGGG CGTTCCGGGA GGTGTGGTCT GGGCGGGACT TGGGAGTGGT CAACCCCTCAG  
421 ATGCTGCATA TAAGCAGCTG CTTTCGCCT GTACTGGTC TCTCTCGGT AACCAGATCT  
481 GAGCCTGGGA GCCCTCTGGC TATCTAGGGA ACCCAGTGC TAAGCCTCAA TAAAGCTTGC  
541 CTTGAGTGCT TTAAGTAGTG TGTGCCATC TGTTGTGTGA CTCTGGTAAAC TAGAGATCCC  
601 TCAGACCCCTT TGTGGTAGTG TGGAAAATCT CTAGCAGTGG CGCCCGAACAA GGGACCAGAA  
661 AGTGAAAGTG AGACCAGAGG AGATCTCTCG ACGCAGGACT CGGCTTGCTG AAGTGCACAC  
721 GGCAAGAGGC GAGAGGGCG GCTGGTAGT ACGCCAATT TACTTGACTA CGGGAGGCTA  
781 GAAGGAGAGA GATGGGTGCG AGAGCGTCAA TATTAAGCGG CGGAAAATTA GATAAATGGG  
841 AAAGAATTAG GTTAAGGCCA GGGGGAAAGA AACATTATAT GTAAAACAT CTAGTATGGG  
901 CAAGCAGGGGA GCTGGAAAGA TTTGCACTTA ACCCTGGCCT GTTAGAAACA TCAGAAGGCT  
961 GTAAACAAAT AATAAAACAG CTACAACCAAG CTCTTCAGAC AGGAACAGAG GAACTTAGAT  
1021 CATTATTCAA CACAGTAGCA ACTCTCTATT GTGTACATAA AGGGATAGAG GTACGAGACA  
1081 CCAAGGAAGC CTTAGACAAG ATAGAGGAAG AACAAAACAA ATGTCAGCAA AAAGCACAAC  
1141 AGGCAAAGC AGCTGACGAA AAGGTCAGTC AAAATTATCC TATAGTACAG AATGCCAAC  
1201 GGCAAATGGT ACACCAAGCT ATATCACCTA GAACATTGAA TGCATGGATA AAAGTAATAG  
1261 AGGAAAAGGC TTTCAATCCA GAGGAAATAC CCATGTTAC AGCATTATCA GAAGGAGCCA  
1321 CCCCCACAAGA TTTAACACA ATGTTAAATA CAGTGGGGGG ACATCAAGCA GCCATGCAA  
1381 TGTTAAAAGA TACCATCAAT GAGGAGGCTG CAGAATGGGA TAGGACACAT CCAGTACATG  
1441 CAGGGCCTGT TGCACCAGGC CAGATGAGAG AACCAAGGGG AAGTGCACATA GCAGGAAC  
1501 CTAGTACCCCT TCAGGAACAA ATAGCATGGA TGACAAGTAA TCCACCTATT CCAGTAGAAG  
1561 ACATCTATAA AAGATGGATA ATTCTGGGT TAAATAAAAT AGTAAGAATG TATAGCCCTG  
1621 TTAGCATTTC GGACATAAAA CAAGGGCCAA AAGAACCCCTT TAGAGACTAT GTAGACCGGT  
1681 CTTTTAAAC CTTAAGAGCT GAACAAGCTA CACAAGATGT AAAGAATTGG ATGACAGACA  
1741 CCTTGTTGGT CAAAATGCG AACCCAGATT GTAAGACCAT TTTAAGAGCA TTAGGACAG  
1801 GGGCCTCATT AGAAGAAATG ATGACAGCAT GTCAGGGAGT GGGAGGACCT AGCCATAAAG  
1861 CAAGAGTGTG GGCTGAGGCA ATGAGCCAAG CAAACAGTAA CATACTAGTG CAGAGAAGCA  
1921 ATTAAAGG CTCTAACAGA ATTATTAAT GTTCAACTG TGGCAAAGTA GGGCACATAG  
1981 CCAGAAATTG CAGGGCCCT AGGAAAAGG GCTGTTGGAA ATGTGGACAG GAAGGACACC  
2041 AAATGAAAGA CTGTACTGAG AGGCAGGCTA ATTGTTTAGG GAAAATTGG CCTTCCCACA  
2101 AGGGGAGGCC AGGGAAATTTC CTCCAGAACAA GACCAGAGCC AACAGCCCCA CCAGCAGAAC  
2161 CAACAGCCCC ACCAGCAGAG AGCTTCAGGT TCGAGGAGAC AACCCCGTG CCGAGGAAGG  
2221 AGAAAGAGAG GGAACCTTA ACTTCCCTCA AATCACTCTT TGGCAGCGAC CCCTTGTCTC  
2281 AATAAAAGTA GAGGGCCAGA TAAAGGAGGC TCTCTTAGAC ACAGGAGCAG ATGATACAGT  
2341 ATTAGAAGAA ATAGATTGTC CAGGGAAATG GAAACCAAAA ATGATAGGGG GAATTGGAGG  
2401 TTTTATCAA GTAAGACAGT ATGATCAAAT ACTTATAGAA ATTGTTGGAA AAAAGGCTAT  
2461 AGGTACAGTA TTAGTAGGGC CTACACCAGT CAACATAATT GGAAGAAATC TGTAACTCA  
2521 GCTGGATGC AACTAAATT TTCCAATTAG TCCTATTGAA ACTGTACCG TAAAATTAAA  
2581 ACCAGGAATG GATGGCCCAA AGGTCAAACA ATGGCCATTG ACAGAAGAAA AAATAAAAGC  
2641 ATTAACAGCA ATTGTTGAGG AAATGGAGAA GGAAGGAAA ATTACAAAAA TTGGCCTGA  
2701 TAATCCATAT AACACTCCAG TATTTGCCAT AAAAAAGAAG GACAGTACTA AGTGGAGAAA  
2761 ATTAGTAGAT TTCAGGAAAC TCAATAAAAG AACTCAAGAC TTTTGGGAAG TTCAATTAGG  
2821 AATACCACAC CCAGCAGGAT TAAAAAAAGAA AAAATCACTG ACAGTGCCTAG ATGTGGGGGA  
2881 TGCATATTTC TCAGTCCCTT TAGATGAAAG CTTCAAGGAAA TATACTGCAT TCACCATACC

FIGURE 11

2941 TAGTATAAAC AATGAAACAC CAGGGATTAG ATATCAATAT AATGTGCTGC CACAGGGATG  
 3001 GAAAGGATCA CCAGCAATAT TCCAGAGTAG CATGACAAAA ATCTTAGAGC CCTTCAGAGC  
 3061 AAAAAATCCA GACATAGTTA TCTATCAATA TATGGATGAC TTGATGAG GATCTGACTT  
 3121 AGAAATAGGG CAACATAGAG CAAAAATAGA AGAGTTAAGG GAACATTTAT TGAAATGGGG  
 3181 ATTTACAACA CCAGACAAGA AACATCAAAA AGAACCCCCA TTTCTTGGG TGGGGTATGA  
 3241 ACTCCATCCT GACAAATGGA CAGTACAACC TATACTGCTG CCAGAAAAGG ATAGTTGGAC  
 3301 TGTCAATGAT ATACAGAAGT TAGTGGGAAA ATTAAACTGG GCAAGTCAGA TTTACCCAGG  
 3361 GATTAAAGTA AGGCAACTCT GTAAACTCCT CAGGGGGGCC AAAGCACTAA CAGACATAGT  
 3421 ACCACTAACT GAAGAAGCAG AATTAGAATT GGCAGAGAAC AGGGAAATT TAAGAGAAC  
 3481 AGTACATGGA GTATATTATG ATCCATCAAA AGACTTGATA GCTGAAATAC AGAACACAGGG  
 3541 GCATGAACAA TGGACATATC AAATTTATCA AGAACCATTT AAAAATCTGA AAACAGGGAA  
 3601 GTATGCAAAA ATGAGGACTA CCCACACTAA TGATGTAAAA CAGTTAACAG AGGCAGTGCA  
 3661 AAAAATAGCC ATGGAAAGCA TAGTAATATG GGGAAAGACT CCTAAATTAA GACTACCCAT  
 3721 CCAAAAAGAA ACATGGGAGA CATGGTGGAC AGACTATTGG CAAGCCACCT GGATCCCTGA  
 3781 GTGGGAGTTT GTTAATACCC CTCCCCTAGT AAAATTATGG TACCAACTAG AAAAAGATCC  
 3841 CATAGCAGGA GTAGAAACTT TCTATGTAGA TGGAGCAACT AATAGGGAAG CTAAAATAGG  
 3901 AAAAGCAGGG TATGTTACTG ACAGAGGAAG GCAGAAAATT GTTACTCTAA CTAACACAAC  
 3961 AAATCAGAAG ACTGAGTTAC AAGCAATTCA GCTAGCTCTG CAGGATTCA GATCAGAAGT  
 4021 AAACATAGTA ACAGACTCAC AGTATGCATT AGGAATCATT CAAGCACAAC CAGATAAGAG  
 4081 TGACTCAGAG ATATTTAACC AAATAATAGA ACAGTTAATA AACAAAGGAAA GAATCTACCT  
 4141 GTCATGGGTAA CCAGCACATA AAGGAATTGG GGGAAATGAA CAAGTAGATA AATTAGTAAG  
 4201 TAAGGGAATT AGGAAAGTGT TGTTCCTAGA TGGAAATAGAT AAAGCTCAAG AAGAGCATGA  
 4261 AAGGTACCAC AGCAATTGGA GAGCAATGGC TAATGAGTT AATCTGCCAC CCATAGTAGC  
 4321 AAAAGAAATA GTAGCTAGCT GTGATAAATG TCAGCTAAAA GGGGAAGCCA TACATGGACA  
 4381 AGTCGACTGT AGTCCAGGG AATGGCAATT AGATTGTACC CATTAGAGG GAAAATCAT  
 4441 CCTGGTAGCA GTCCATGTAG CTAGTGGCTA CATGGAAGCA GAGGTTATCC CAGCAGAAC  
 4501 AGGACAAGAA ACAGCATATT TTATATTAAA ATTACGAGGA AGATGGCCAG TCAAAGTAAT  
 4561 ACATACAGAC AATGGCAGTA ATTTTACCA GACTGAGTT AAGGCAGCTT GTTGGTGGGC  
 4621 AGGTATCCAA CAGGAATTG GAATTCCCTA CAATCCCCA AGTCAGGGAG TGGTAGAATC  
 4681 CATGAATAAA GAATTAAAGA AAATAATAGG ACAAGTAAGA GATCAAGCTG AGCACCTTAA  
 4741 GACAGCAGTA CAAATGGCAG TATTCAATTCA CAATTAAAGG GAAAAGGGG GAATTGGGG  
 4801 GTACAGTGCA GGGGAAAGAA TAATAGACAT AATAGCAACA GACATACAAA CTAAAGAATT  
 4861 ACAAAAACAA ATTATAAGAA TTCAAAATT TCAGGTTTAT TACAGAGACA GCAGAGACCC  
 4921 TATTGGAAA GGACCAGCCG AACTACTCTG GAAAGGTGAA GGGGTAGTAG TAATAGAAGA  
 4981 TAAAGGTGAC ATAAAGGTAG TACCAAGGAG GAAAGCAAAA ATCATTAGAG ATTATGGAAA  
 5041 ACAGATGGCA GGTGCTGATT GTGTGGCAGG TGGACAGGAT GAAGATTAGA GCATGGAATA  
 5101 GTTTAGTAA GCACCATATG TATATATCAA GGAGAGCTAG TGGATGGGT TACAGACATC  
 5161 ATTTGAAAG CAGACATCCA AAAGTAAGTT CAGAACTACA TATCCCATTA GGGGATGCTA  
 5221 GATTAGTAAT AAAACATAT TGGGGTTTCAGA AGACAGGAGA AAGAGATTGG CATTGGGT  
 5281 ATGGAGTCTC CATAGAATGG AGACTGAGAG AATACAGCAC ACAAGTAGAC CCTGACCTGG  
 5341 CAGACCAGCT AATTCACTG CATTATTTG ATTGTTTAC AGAATCTGCC ATAAAGACAAG  
 5401 CCATATTAGG ACACATAGTT TTTCTCTAGGT GTGACTATCA AGCAGGACAT AAGAAGGTAG  
 5461 GATCTCTGCA ATACTTGGCA CTGACAGCAT TGATAAAACC AAAAAAGAGA AAGCCACCTC  
 5521 TGCTTAGTGT TAGAAAATTA GTAGAGGATA GATGGAACGA CCCCCAGAAC ACCAGGGGCC  
 5581 GCAGAGGGAA CCATACAATG AATGGACACT AGAGATTCTA GAAGAACTCA AGCAGGAAGC  
 5641 TGTCAATGAT ATACAGAAGT TAGTGGGAAA ATTAAACTGG GCAAGTCAGA TTTACCCAGG  
 5701 TGGGGATACT TGGACGGGAG TTGAAGCTAT AATAAGAGTA CTGCAACAAAC TACTGTTCAT  
 5761 TCATTTCAGA ATTGGATGCC AACATAGCAG AATAGGCATC TTGCGACAGA GAAGAGCAAG  
 5821 AAATGGGAGCC AGTAGATCCT AACTAAAGC CCTGGAACCA TCCAGGAAGC CAACCTAAAA  
 5881 CAGCTTGTAA TAATTGCTTT TGCAAAACACT GTAGCTATCA TTGCTAGTT TGCTTTCAGA

FIGURE 11

5941 CAAAAGGTTT AGGCATTTCC TATGGCAGGA AGAAGCGGAG ACAGCGACGA AGCGCTCCTC  
6001 CAAGTGGTGA AGATCATCAA AATCCTCTAT CAAAGCAGTA AGTACACATA GTAGATGTAA  
6061 TGGTAAGTTT AAGTTTATTAAAGGAGTAG ATTATAGATT AGGAGTAGGA GCATTGATAG  
6121 TAGCACTAAT CATAAGCAATA ATAGTGTGGA CCATAGCATA TATAGAATAT AGGAATTGG  
6181 TAAGACAAAA GAAAATAGAC TGGTTAATTAAAGAATTAG GGAAAGAGCA GAAGACAGTG  
6241 GCAATGAGAG TGATGGGAC ACAGAAGAAT TGTCAACAAT GGTGGATATG GGGCATCTTA  
6301 GGCTTCTGGA TGCTAATGAT TTGTAACACG GAGGACTTGT GGGTCACAGT CTACTATGGG  
6361 GTACCTGTGT GGAGAGAAGC AAAAACTACT CTATTCTGTG CATCAGATGC TAAAGCATAT  
6421 GAGACAGAAG TGCATAATGTC TGGGCTACA CATGCTTGTG TACCCACAGA CCCCCAACCCA  
6481 CAAGAAATAG TTTTGGGAAA TGTAACAGAA AATTTTAATA TGTGGAAAAA TAACATGGCA  
6541 GATCAGATGC ATGAGGATAT ATCAGTTA TGGGATCAA GCCTAAAGCC ATGTGTAAAG  
6601 TTGACCCCCAC TCTGTGTCACTTAAACTGT ACAGATACAA ATGTTACAGG TAATAGAACT  
6661 GTTACAGGTA ATACAAATGA TACCAATATT GCAAATGCTA CATATAAGTA TGAAGAAATG  
6721 AAAAATTGCT CTTTCAATGCAACCACAGAA TTAAGAGATA AGAACATAA AGAGTATGCA  
6781 CTCTTTATA AACTTGATAT AGTACCACTT AATGAAAATA GTAACAACCT TACATATAGA  
6841 TTAATAAATT GCAATACCTC AACCATAACA CAAGCCTGTC CAAAGGTCTC TTTTGACCCG  
6901 ATTCCTATAC ATTACTGTGC TCCAGCTGAT TATGCGATTC TAAAGTGTAA TAATAAGACA  
6961 TTCAATGGGA CAGGACCATG TTATAATGTC AGCACAGTAC AATGTACACA TGGATTAAAG  
7021 CCAGTGGTAT CAACTCAACT ACTGTTAAAT GGTAGTCTAG CAGAAGAAGG GATAATAATT  
7081 AGATCTGAAA ATTTGACAGA GAATACCAAA ACAATAATAG TACATCTTAA TGAATCTGTA  
7141 GAGATTAAATT GTACAAGGCC CAACAATAAT ACAAGGAAAA GTGTAAGGAT AGGACCAAGGA  
7201 CAAGCATTCT ATGCAACAAA TGACGTAATA GGAAACATAA GACAAGCACA TTGTAACATT  
7261 AGTACAGATA GATGGAATAA AACTTTACAA CAGGTAAATGA AAAAATTAGG AGAGCATTTC  
7321 CCTAATAAAA CAATAAAATT TGAACCACAT GCAGGAGGGG ATCTAGAAAT TACAATGCAT  
7381 AGCTTIAATT GTAGAGGAGA ATTTTCTAT TGCAATACAT CAAACCTGTT TAATAGTACA  
7441 TACTACCCCTA AGAATGGTAC ATACAAATAC AATGTAATT CAAGCTTACCATCACACTC  
7501 CAATGCAAAA TAAAACAAAT TGTACGCTG TGGCAAGGGG TAGGACAAGC AATGTATGCC  
7561 CCTCCCATTG CAGGAAACAT AACATGTAGA TCAAACATCA CAGGAATACT ATTGACACGT  
7621 GATGGGGGAT TTAACAAACAC AAACAACGAC ACAGAGGAGA CATTCAAGACC TGGAGGAGGA  
7681 GATATGAGGG ATAACCTGGAG AAGTGAATTATAAAATATA AAGTGGTAGA AATTAAGCCA  
7741 TTGGGAATAG CACCCACTAA GGCAAAAGA AGAGTGGTGC AGAGAAAAAA AAGAGCAGTG  
7801 GGAATAGGAG CTGTGTTCTG TGGGTTCTG GGACGAGCAG GAAGCACTAT GGGCGCAGCG  
7861 TCAATAACCGC TGACGGTACA GGCCAGACAA CTGTTGTCG GTATAGTGCA ACAGCAAAGC  
7921 AATTGCTGA AGGCTATAGA GGCGCAACAG CATATGTTGC AACTCACAGT CTGGGGCATT  
7981 AAGCAGCTCC AGGCGAGAGT CCTGGCTATA GAAAGATACC TAAAGGATCA ACAGCTCCTA  
8041 GGGATTTGGG GCTGCTCTGG AAGACTCATC TGCAACACTG CTGTCCTG GAACTCCAGT  
8101 TGGAGTAATA AATCTGAAAGC AGATATTGG GATAACATGA CTTGGATGCA GTGGGATAGA  
8161 GAAATTAAATA ATTACACAGA AACAAATATTC AGGTTGCTTG AAGACTCGCA AAACCAGCAG  
8221 GAAAAGAATG AAAAAGATT ATTAGAATTG GACAAGTGGATAATCTGTG GAATTGGTTT  
8281 GACATATCAA ACTGGCTGTG GTATATAAAATATTACATAA TGATAGTAGG AGGCTTGATA  
8341 GTTTTAAGAA TAATTTTGCTG TGTGCTCTCT ATAGTGAATA GAGTTAGGCA GGGATACTCA  
8401 CCTTTGTCAT TTCAAGACCT TACCCCAAGC CCGAGGGGAC TCGACAGGCT CGGAGGAATC  
8461 GAAGAAGAAG GTGGAGAGCA AGACAGAGAC AGATCCATAC GATTGGTAGG CGGATTCTTG  
8521 TCGCTTGCCCT GGGACGATCT GCGGAGCCTG TGCCCTTCTCA GCTACCACCG CTTGAGAGAC  
8581 TTCATATTAA TTGCAAGTGGAG GGCAGTGGAA CTTCTGGGAC ACAGCAGTCT CAGGGGACTA  
8641 CAGAGGGGGT GGGAGATCCT TAAGTATCTG GGAAGTCTTG TGCAGTATTG GGGCTAGAG  
8701 CTAAAAAAGA GTGCTATTAG TCCGCTTGAT ACCATAGCAA TAGCAGTAGC TGAAGGAACA  
8761 GATAGGATTA TAGAATTGGT ACAAAAGAATT TGTAGAGCTA TCCTCAACAT ACCTAGGAGA  
8821 ATAAGACAGG GCTTTGAAGC AGCTTGTCA TAAAATGGGA GGCAAGTGGT CAAAACGCAG  
8881 CATAGTTGGA TGGCCTGCAG TAAGAGAAAG AATGAGAAGA ACTGAGCCAG CAGCAGAGGG  
8941 AGTAGGAGCA GCGTCTCAAG ACTTAGATAG ACATGGGGCA CTTACAAGCA GCAACACACC

**FIGURE 11**

9001 TGCTACTAAT GAAGCTTGTG CCTGGCTGCA AGCACAAAGAG GAGGACGGAG ATGTTAGGCTT  
9061 TCCAGTCAGA CCTCAGGTAC CTTAAGACCA AATGACTTAT AAGAGTGCAG TAGATCTCAG  
9121 CTTCTTTTA AAAGAAAAGG GGGGACTGGA AGGGTTAATT TACTCTAGGA AAAGGCAAGA  
9181 AATCCTTGAT TTGTGGGTCT ATAACACACAA AGGCTTCTTC CCTGATTGGC AAAACTACAC  
9241 ATCGGGGCCA GGGGTCCGAT TCCCACGTGAC CTTTGGATGG TGCTTCAAGC TAGTACCAAGT  
9301 TGACCCAAGG GAGGTGAAAG AGCCAATGA AGGAGAAAGAC AACTGTTGC TACACCCAT  
9361 GAGCCAACAT GGAGCAGAGG ATGAAGATAG AGAAGTATTA AAGTGGAAAGT TTGACAGCCT  
9421 TCTAGCACAC AGACACATGG CCCCGAGCT ACATCCGGAG TATTACAAAG ACTGCTGACA  
9481 CAGAAAGGGAC TTTCCGCCTG GGACTTTCCA CTGGGGCGTT CCGGGAGGTG TGGTCTGGC  
9541 GGGACTTGGG AGTGGTCACC CTCAGATGCT GCATATAAGC AGCTGTTTT CGCTTGTACT  
9601 GGGTCTCTCT CGGTAGACCA GATCTGAGCC TGGGAGCTCT CTGGCTATCT AGGGAACCCA  
9661 CTGCTTAGGC CTCATAAAAG CTTGCCTTGA GTGCTCTAAG TAGTGTGTGC CCATCTGTTG  
9721 TGTGACTCTG GTAACTAGAG ATCCCTCAGA CCCTTGTGG TAGTGTGGAA AATCTCTAGC  
9781 A

FIGURE 11

**SEQ ID NO:34**

GCTGAGGCAATGAGCCAAGCAACCAGCGCAAACATACTGATGCAGAGAAGCAATT  
CAAAGGCCCTAAAAGAATTATTAAATGTTCAACTGTGGCAAGGAAGGGCACATAG  
CTAGAAATTGTAGGGCCCCTAGGAAAAAAGGCTGTTGGAAATGTGGAAAGGAAGGA  
CACCAAATGAAAGACTGTACTGAGAGGCAGGCTAA

**FIGURE 12**

975Pol wt until 6aa Int: (SEQ ID NO:35)

TTTTTAGGAAAGATTGGCCTCCCACAAGGGAAAGGCCAGGGATTCCCTCAGAA  
CAGAACAGAGCCAACAGCCCCACCAGCAGAGAGCTCAAGTCGAGGAGACAACCC  
CCGCTCCGAAGCAGGAGCCAAAGACAGGGAAACCTTAATTCCCTCAAATCACTCT  
TTGGCAGCGACCCCTTGTCTCAATAAAAGTAGGGGTCAAATAAAGGAGGCTCTCT  
AGACACAGGGAGCTGATGATACAGTATTAGAAGAAATGAGTTGCCAGGAAAATGGA  
AACCAAAAATGATAGGGAGGATTGGAGGTTTATCAAAGTAAGACAGTATGATCAA  
ATACCTATAGAAATTGTGGAAAAAGGCTATAGGTACAGTATTAATAGGACCTACA  
CCTGTCAACATAATTGGAAGGAATATGTTGACTCAGCTGGATGCACACTAAATT  
CCAATTAGTCCCATTGAAACTGTGCCAGTAAAATTAAAGCCAGGAATGGATGGCCA  
AAGGTTAAACAATGCCATTGACAGAAGAGAAAATAAAGCATTACAGCAATTG  
TGAAGAAATGGAGAAAGAAGGAAAATTACAAAATTGGGCCTGAAAATCCATATA  
ACACTCCAGTATTGCCATAAAAAGAAGGACAGTACTAAGTGGAGAAAGTTAGTA  
GATTTCAGGGAACTTAATAAAAGAACTCAAGACTTTGGGAAGTCAATTAGGAATA  
CCACACCCAGCAGGGTAAAAAGAAAAATCAGTGACAGTACTGGATGTGGGGA  
TGCATATTTTCAGTTCTTATAGTGAGGACTTCAGGAATATACTGCATTACCCATA  
CCTAGTATAAAACAATGAAACACCAGGGATTAGATATCAATATAATGTGCTTCACAG  
GGATGGAAAGGATCACCATCAATATTCCAGAGTAGCATGACAAAAATCTAGAGCC  
CTTAGAGCAAGAAATCCAGAAATAGTCATCTATCAATATATGGATGACTGTATGT  
AGGATCTGACTTAGAAATAGGGCAACATAGAGCAAAATAGAGGAGTTAAGAAAAC  
ATCTGTTAAGGTGGGATTACACACCGGACAAGAAACATCAGAAAGAACCCCCCA  
TTCTTGGATGGGTATGAACTCCATCCTGACAAATGGACAGTACAGCCTATAGAG  
TTGCCAGAAAAGGAAAGCTGGACTGTCAATGATATAACAGAAGTTAGTGGAAAATT  
AAATTGGGCCAGTCAGATTACCCAGGAATTAAAGTAAGGCAACTTGTAAACTCCT  
TAGGGGGCCAAGCACTAACAGATATAGTACCAACTGAAGAACAGAGAATTAG  
AATTGGCAGAGAACAGGGAAATTCTAACAGAGAACAGCAGTACATGGAGTATTATGAC  
CCATCAAAAGACTTGGTAGCTGAAATACAGAAACAGGGCATGACCAATGGACATA  
TCAAATTACCAAGAACATTCAAAAACCTGAAAACAGGGAGTATGCAAAATGA  
GGACTGCCACACTAATGATGTTAACAGAGGCAGTGCAAAAAATAGCT  
ATGGAAAGCATAGTAATATGGGAAAGACTCCTAAATTAGACTACCCATCCAAA  
AGAAACATGGGAGACATGGTAGCAGACTATTGGCAAGCCACCTGGATTCTGAGT  
GGGAGTTGTTAACCCCTCCCTAGTAAATTATGGTACAGCTAGAGAAAGAAC  
CCATAATAGGAGCAGAAACTTCTATGTAGATGGAGCAGCTAACAGGGAAACTAAA  
ATAGGAAAAGCAGGGTATGTTACTGACAGAGGAAGGCAGAAAATTGTTCTCTAAC  
AGAAACAACAAATCAGAAGACTGAATTACAAGCAATTCAAGCTAGCTTGCAGATT  
AGGATCAGAAGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCATTCAAG  
CACAAACCAGATAAGAGTGAATCAGAGTTAGTCACCAATAATAGAACAAATTAA  
AAAAAGGAAAAGGTCTACCTGTACGGTACCAAGCAGCACATAAAGGAATTGGAGGAAA  
TGAACAAATAGATAAATTAGTAAGTAAGGAAATCAGGAAAGTGCTTTCTAGATG  
GAATAGAT

FIGURE 13

**SEQ ID NO:36**

GGCGGCATCGT GATCT ACCAGTACATGGACGACCTGTACGTGGGCAGCGGCG  
GC

**FIGURE 14**

SEQ ID NO: 37

GGIVIYQYMDDLYVGSGG

## FIGURE 15

TGGAAAGGGTTAATTACTCCAGGAAAAGGCAAGAGATCCTGATTATGGGTCTATC  
ACACACAAGGCTACTCCCTGATTGGCAAAACTACACACCGGGACCAGGGTCAGA  
TATCCACTGACCTTGGATGGTCTCAAGCTAGTGCCAGTTGACCCAAGGGAAAGTA  
GAAGAGGCCAACGGAGGAGAAGACAACCTGTTGCTACACCCTATGAGCCAGTATGG  
AATGGATGATGAACACAAAGAAGTGTACAGTGGAAAGTTGACAGCAGCCTAGCAC  
GCAGACACCTGGCCCGAGCTACATCCGGATTATTACAAAGACTGCTGAÇACAGA  
AGGGACTTCCGCCTGGACTTCCACTGGGGCGTCCAGGGGGAGTGGTCTGGCG  
GGACTGGGAGTGGCCAGCCCTCAGATGCTGCATATAAGCAGCGGCTTCTGCTGTA  
CTGGGTCTCTAGGTAGACCAGATCCGAGCCTGGGAGCTCTGTCTATCTGGG  
ACCCACTGCTTAGGCCTCAATAAGCTGCCTGAGTGCTCTAAGTAGTGTGTGCC  
ATCTGTTGTTGACTCTGTAACCTCTGTAACTAGAGATCCCTCAGACCCTTGTGGT  
AGTGTGGAAAATCTCTAGCAGTGGCGCCGAACAGGGACTTGAAGTGCACCTGGCAAGAG  
ACCAAGAGAAGATCTCTGACCGCAGGACTCGGCTTGCTGAAGTGCACCTGGCAAGAG  
GCGAGGGGGCGACTGGTGAGTACGCCAAAATTGGTACTAGCGGAGGCTAGA  
AGGAGAGAGATGGGTGCGAGAGCGTCAATATTAAAGAGGGGAAAATTAGACAAAT  
GGGAAAAAAATTAGGTACGCCAGGGGGAGAAAACACTATATGCTAAAACACCTA  
GTATGGGCAAGCAGAGAGCTGGAAAGATTGCAGTTAACCCTGGCCTTGTAGAGAC  
ATCAGACGGATGTAGAC AAATAATAAAACAGCTACAACCAGCTCTCAGA  
CAGGAACAGAGGAATTAGATCATTATTAAACACAGTAGCAACTCTCTATTGTGTAC  
ATAAAGGGATAGATGTACGAGACACCAAGGAAGCCTAGACAAGATAGAGGAGGA  
ACAAAACAAATGTCAGCAAAAAACACAGCAGCGGAAGCGGCTGACAAAAAGGTC  
AGTCAAAATTATCCTATAGTGCAGAACCTCCAAGGGCAATGGTACACCAGGCCAT  
ATCACCTAGAACCTTGAATGCATGGTAAAAGTAATAGAGGAGAAGGCTTTAGCC  
CAGAGGTAATACCCATGTTACAGCATTATCAGAAGGAGCCACCCCACAAGATT  
AACACCATGTTAAATACAGTGGGGGACATCAAGCAGCCATGCAAATGTTAAAG  
ATACCATCAATGAGGAGGCTGCAGAATGGGATAGTTACATCCAGTACATGCAGGG  
CCTGTTGCACCAGGCCAGATGAGAGAACCAAGGGGAAGTGACATAGCAGGAAC  
CTAGTACCCCTCAAGAACAAATAGCATGGATGACAAGTAACCCACCTATCCCAGTA  
GGGGACATCTATAAAAGGTGGATAATTCTGGGTTAAATAAAATAGTAAGAATGTA  
CAGCCCTGTCAGCATTAGACATAAAACAAGGACCAAAGGAACCCCTTAGAGACT  
ATGTAGACCGGTTCTCAAAACTTAAGAGCTGAACAACTACACAAGAGGTAAAA  
AATTGGATGACAGACACCTGTTAGTCCAAAATGCGAACCCAGATTGTAAGACCATT  
TTAAGAGCATTAGGACCAGGGCTTCATTAGAAGAAATGATGACAGCATGTCAGGG  
AGTGGGAGGACCTAGCCACAAAGCAAGAGTTGGCTGAGGCAATGAGCCAAGCAA  
ACAATACAAGTGTAAATGATACAGAAAAGCAATTAAAGGCCCTAGAAGAGCTGTT  
AAATGTTCAACTGTGGCAGGGCACATAGCCAGGAATTGCAGGGCCCTAG  
GAAAAGGGCTGTTGGAAATGTGGAAAGGAAGGACACCAAATGAAAGACTGTACT  
GAGAGGCAGGCTAATTGGAAAATTGGCTTCCCACAAGGGGAGGCCAGG  
GAATTCCCTCAGAGCAGACAGAGCCAACAGCCCCACCAACTAGAACCAACAGCCC  
CACCAGCAGAGAGCTCAAGTTCAAGGAGACTCCGAAGCAGGAGGCCAAAGACAG  
GGAACCTTAACTCCCTCAAATCACTTTGGCAGCGACCCCTGTCTCAATAAAA

## FIGURE 16

GTAGCGGGCAAACAAAGGAGGCTTTAGATAACAGGAGCAGATGATAACAGTACT  
AGAAGAAATAAAGTGCAGGAAAATGGAAACCAAAATGATAGGAGGAATTGGA  
GGTTTATCAAAGTAAGACAGTATGATCAAATACTTATAGAAATTGTGGAAAAAGG  
GCTATAGGTACAGTATTAGTAGGACCTACACCTGTCAACATAATTGGAAGAAATCTG  
TTGACTCAGCTGGATGCACACTAAATTCCAATTAGCCCCATTGAAACTGTACCA  
GTAAAATTAAAGCCAGGAATGGATGGCCAAAGGTTAAACAATGCCATTGACAGA  
AGAAAAAAATAAAGCATTAACAGAAATTGTGAGGAATGGAGAAGGAAGGAAAA  
ATTACAAAAATTGGGCCTGAAAATCCATATAACACTCCAGTATTGCCATAAAGAAG  
AAGGACAGTACAAAGTGGAGAAAATTAGTAGATTCAAGGAACTCAATAAAAGAAC  
TCAAGACTTTGGGAAGTCCAATTAGGAATACCAACACCCAGCAGGGTTAAAAAAGA  
AAAAATCAGTACAGTACTGGATGTGGAGATGCATATTTCAGTCCCTTAGATG  
AGAGCTTCAGAAATATACTGCATTCAACACTACAGTATAAACAAATGAAACACCA  
GGGATTAGATATCAATATAATGTTCTCACAGGGATGGAAAGGATCACCAGCAA  
TATTCCAGAGTAGCATGACAAGAATCTTAGAGCCCTTAGAACACAAAACCCAGAA  
GTAGTTATCTATCAATATATGGATGACTTATATGTAGGATCTGACTTAGAAATAGGG  
CAACATAGAGCAAAATAGAGGAGTTAAGAGGACACCTATTGAAATGGGGATTAC  
CACACCAGACAAGAACATCAGAAAGAACCCCCATTCTTGATGGGTATGAAC  
TCCATCCTGACAAATGGACAGTACAGCCTATACAGCTGCCAGAAAAGGAGAGCTGG  
ACTGTCAATGATATACAGAAGTTAGTGGAAAGTAAACTGGCAAGTCAGATT  
CCCAGGGATTAAAGTAAGGCAACTGTGTAAACTCCTTAGGGAGCCAAAGCACTAA  
CAGACATAGTCCACTGAAGAACAGAATTAGAATTGGCTGAGAACAGGGA  
AATTCTAAAAGAACCAAGTACATGGAGTATTATGACCCATCAAAAGATTAAATAG  
CTGAAATACAGAAACAGGGATGACCAATGGACATATCAAATTACCAAGAAC  
ATTAAAAATCTGAGAACAGGAAAGTATGCAAAATGAGGACTGCCACACTAATG  
ATGTGAAACAGTTAGCAGAGGCAGTGCAAAAGATAACCCAGGAAAGCATAGTAATA  
TGGGGAAAAACTCCTAAATTAGACTACCCATCCAAAAGAAACATGGGAGACATG  
GTGGTCAGACTATTGGCAAGCCACCTGGATTCTGAGTGGAGTTGTCAATACCC  
TCCCCTAGTAAATTGTGGTACCAAGCTGGAAAAAGAACCCATAGTAGGGCAGAAA  
CTTCTATGTAGATGGAGCAGCCAATAGGGAAACTAAAATAGGAAAGCAGGGTAT  
GTCACTGACAAAGGAAGGCAGAAAGTTGTTCTCACTGAAACAAACAAATCAGAA  
GACTGAATTACAAGCAATTCAAGCTAGCTTGCAGGATTCAAGGCCAGAAGTAAACA  
TAGTAACAGACTCACAGTATGCATTAGGAATCATTCAAGCACAACCAAGATAAGAGT  
GAATCAGAATTAGTCAGTCAAATAATAGAACAGTTGATAAAAAGGAAAAAGTCTA  
CCTATCATGGTACCAAGCACATAAAGGAATTGGAGGAAATGAACAAGTAGACAAAT  
TAGTAAGTAGTGGAAATCAGAAAAGTACTGTTCTAGATGGAATAGATAAAGCTCAA  
GAAGAGCATGAAAAATATCACAGCAATTGGAGAGCAATTGGCTAGTGAATTAAATCT  
GCCACCCATAGCAGGAAATAGTAGCCAGCTGTGATAAATGTCAGCTAAAG  
GGGAAGCCATGCATGGACAAGTCAGTCTAGTCCAGGAATATGCCAATTAGACTGT  
ACACATTAGAAGGAAAATCATCCTAGTAGCAGTCCATGTAGCCAGTGGCTACAT  
GGAAGCAGAGGTTATCCCAGCAGAAACAGGACAAGAACAGCATACTTATACTAA  
AATTAGCAGGAAGATGGCCAGTCAAAGTAATACATACAGATAATGGCAGTAATT  
ACCAAGTACCGCAGTTAAGGCAGCCTGTTGGTGGCAGATATCCAACGGGAATTG  
AATTCCCTACAATCCCCAAAGTCAAGGAGTAGTAGAACATGAATAAAGAATTAA

FIGURE 16

AGAAAATCATAGGGCAAGTAAGAGATCAAGCTGAGCACCTAACAGACAGCAGTACAA  
ATGGCAGTATTCAATTACAATTTAAAAGAAAAGGGGGGATTGGGGGTACAGTGC  
AGGGGAGAGAATAATAGACATAATAGCATCAGACATACAAACTAAAGAATTACAAA  
AACAAATTATAAAAATTCAAAATTTCGGGTTATTACAGAGACAGCAGAGACCC  
TTGGAAAGGACCAGCCAAACTACTCTGGAAAGGTGAAGGGCAGTAGTAATACAA  
GATAATAGTGTATAAAGGTAGTACCAAGAAGGAAAGCAAAAATCATTAGGACTA  
TGGAAAACAGATGGCAGGTGCTGATTGTGTCAGGTAGACAGGATGAAGATTAGA  
ACATGGCACAGTTAGTAAAGCACCATATGTATGTTGAGGAGAGCTGATGGATGG  
TTCTACAGACATCATTGAAAGCAGACACCCAAAAGTAAGTTCAGAAGTACACAT  
CCCATTAGGAGATGCCAGGTTAGTAATAAAAACATATTGGGGTCTGCAGACAGGAG  
AAAGAGCTTGCATTGGTCACGGAGTCTCCATAGAATGGAGATTGAGAAGATAT  
AGCACACAAAGTAGACCCCTGACCTGACAGACCAACTAATTCAATATGCATTATTTGAT  
TGTGACTATCAAGCAGGACATAACAAGGTAGGATCTCTACAATACTGGCACTGA  
CAGCATTGATAAAACCAAAAAAGATAAAGCCACCTCTGCCTAGTGTAGGAAATT  
GTAGAGGATAGATGGAACAAGCCCCAGAAGACCAGGGGCCGAGAGGAACCATA  
CAATGAATGGACACTAGAGCTTTAGAAGAACTCAAGCAGGAAGCTGTCAGACACT  
TTCCTAGACCATGGCTCCATAACTTAGGACAACATATCTATGAAACCTATGGAGATA  
CTTGGACAGGAGTTGAAGCAATAATAAGAATCCTGCAACAATTACTGTTATTCA  
TCAGGATTGGGTGCCATCATAGCAGAATAGGCATTGCGACAGAGAAGAGCAAGA  
AATGGAGCCAATAGATCCTAACCTAGAACCTGGAACCATCCAGGAAGTCAGCCTA  
AAACTGCTGTAATGGGTGTTACTGTAAACGTTGCAGCTATCATTGTCTAGTTGCTT  
TCAGAAAAAAGGCTTAGGCATTACTATGGCAGGAAGAACGGAGACAGCGACGAA  
GCGCTCCTCCAAGCAATAAAGATCATCAAGATCCTCTACCAAAAGCAGTAAGTACCG  
AATAGTATATGTAATGTTAGATTAACTGCAAGAATAGATTCTAGATTAGGAATAGG  
AGCATTGATAGTAGCACTAATCATAGCAATAATAGTGTGGACCATAGTATATAG  
AATATAGGAAATTGGTAAGGCAAAGGAAAATAGACTGGTAGTTAAAAGGATTAGG  
GAAAGAGCAGAAGACAGTGGCAATGAGAGCGAGGGGACTGAAAGAATTATCGA  
CACTGGTGGATATGGGCATCTTAGGCTTGGATGCTAATGATGTGTAATGTGAA  
GGGCTTGTGGGTACAGTCTACTACGGGGTACCTGTGGGGAGAGAAGCAAAA  
ACTCTATTTGTGCATCAGATGCTAAAGCATATGAGAAAGAAGTCATAATGTCTG  
GGCTACACATGCCTGTGACCCACAGACCCACACAGAAGTGAATTGGC  
AATGTAACAGAAAATTAAACATGTGGAAAATGACATGGGATCAGATGCAGG  
AAGATATAATCAGTTATGGGATCAAAGCCTAACGCCATGTGTAATTGACCC  
CTCTGTGTCACTTAAACTGTACAAATGCAACTGTGTTAACTACAATAACCTCTAA  
GACATGAAAATTGCTCTTATGTAACCACAGAATTAGAGAGATAAGAAAAAGAA  
AGAAAATGCACTTTTATAGACTGTGATATAGTACCACTTAATAATAGGAAGAATGG  
GAATATTAACAACATAGATTAATAAATTGTAATACCTCAGCCATAACACAAGCCTG  
TCCAAAAGTCTGTTGACCCAATTCTATACATTATTGTGCTCCAGCTGGTTATGCG  
CCTCTAAAATGTAATAATAAGAAATTCAATGGAATAGGACCATGCGATAATGTCAG  
CACAGTACAATGTACACATGGAATTAGCCAGTGGTATCAACTCAATTACTGTTAA  
TGGTAGCCTAGCAGAAGAAGAGATAATAATTAGATCTGAAAATCTGACAAACAATG  
TCAAAACAATAATAGTACATCTTAATGAATCTAGAGATTAAATGTACAAGACC

FIGURE 16

TGGCAATAATAACAAGAAAGAGTGTGAGAATAGGACCAGGACAAGCATTCTATGCA  
ACAGGAGACATAATAGGAGATATAAGACAAGCACATTGTAACATTAGTAAAAATGA  
ATGGAATACAACCTTACAAAGGGTAAGTCAAAATTACAAGAACCTCTCCCTAATA  
GTACAGGGATAAAATTGCACCAACTCAGGAGGGACCTAGAAATTACTACACAT  
AGCTTAATTGTGGAGGAGAATTCTATTGCAATACAACAGACCTGTTAATAGT  
ACATACAGTAATGGTACATGCACTAATGGTACATGCATGTCTAATAATACAGAGCG  
CATCACACTCCAATGCAGAATAAAACAAATTATAAACATGTGGCAGGAGGTAGGAC  
GAGCAATGTATGCCCTCCATTGCAGGAAACATAACATGTAGATCAAATATTACA  
GGACTACTATTAAACACGTGATGGAGGAGATAATAACTGAAACAGAGACATTAG  
ACCTGGAGGAGGAGACATGAGGGACAATTGGAGAAGTGAATTATATAAATACAAG  
GTGGTAGAAATTAAACCATTAGGAGTAGCACCCACTGCTGAAAAAGGAGAGTGGT  
GGAGAGAGAAAAAGAGCAGTAGGAATAGGAGCTGTCTGGGTCTGGAG  
CAGCAGGAAGCACTATGGCGCAGCATCAATAACGCTGACGGTACAGGCCAGACAA  
TTATTGTCTGGTATAGTGCACAGCAAAGTAATTGCTGAGGGCTATAGAGGCAGCAA  
CAGCATATGTTGCAACTCACGGTCTGGGCATTAAGCAGCTCCAGGCAAGAGTCCTG  
GCTATAGAGAGATACCTACAGGATCAACAGCCTAGGACTGTGGGCTGCTCTGG  
AAAACATCTGCACCAACTATGTGCTTGGAACTCTAGTGGAGTAATAAAACTCA  
AAAGTGTATTGGATAACATGACCTGGATGCAGTGGATAGGAAATTAGTAATT  
ACACAAACACAATATAACAGGTTGCTGAAGACTCGCAAAGCCAGCAGGAAAGAAA  
TGAAAAAGATTACTAGCATTGGACAGGTGGAACAATCTGTGGAATTGGTTAGCAT  
AACAAATTGGCTGTGGTATATAAAATATTCTATAATGATAGTAGGAGGCTGATAG  
GTTAAGAATAATTGCTGTGCTCTCTAGTAAATAGAGTTAGGCAGGGATACT  
CACCCTTGTCAATTGCAGACCCCTATCCCAAACCCGAGGGGACCCGACAGGCTCGGA  
GGAATCGAAGAAGAAGGTGGAGAGCAAGACAGCAGCAGATCCATTGATTAGTGA  
GCGGATTCTTGACACTTGCCTGGGACGACCTACGAAGCCTGTGCCTCTGCTACC  
ACCGATTGAGAGACTTCATATTAAATTGAGTAGTGAGAGCAGTGGAACTCTGGGACAC  
AGTAGTCTCAGGGGACTGCAGAGGGGTGGGAACCCCTAAGTATTGGGAGTCT  
TGTGCAATATTGGGGCTAGAGTAAAAAGAGTGTCTTAAATCTGCTTGATACTAT  
AGCAATAGCAGTAGCTGAAGGAACAGATAGGATTCTAGAATTCTACACAAACCTTT  
GTAGAGGTATCCGCAACGTACCTAGAAGAATAAGACAGGGCTCGAAGCAGCTTG  
CAATAAAATGGGGGCAAGTGGCAAAAGCAGTATAATTGGATGGCCTGAAGTAA  
GAGAAAGAATCAGACGAACACTAGGTCAAGCAGCAGAGGGAGTAGGATCAGCGTCTCA  
AGACTTAGAGAAACATGGGCACCTACAACCAGCAACACAGCCCACAACAATGCTG  
CTTGCCTGGCTGGAAGCGCAAGAGGAGGAAGGAGAAGTAGGCTTCCAGTCAGA  
CCTCAGGTACCTTAAGACCAATGACTTAAAGCAGCAATAGATCTCAGCTCTT  
TTAAAAGAAAAGGGGGACTGGAAGGGTTAATTACTCCAAGAAAAGGCAAGAGAT  
CCTGATTGTGGTTATAACACACAAGGCTTCCCTGATTGGCAAAACTACAC  
ACCGGGACCAGGGTCAGATTCCACTGACCTTGGATGGTACTTCAAGCTAGAGCC  
AGTCGATCCAAGGGAAAGTAGAAGAGGCCAATGAAGGAGAAAACAACAGTAACT  
ACCTATGCCAGCATGGAATGGAGGATGAAGACAGAGAAGTATTAGATGGAAG  
TTGACAGTACGCTAGCACGCAGACACATGGCCCGCAGCTACATCCGGAGTATTAC  
AAAGACTGCTGACACAGAAGGGACTTCCGCTGGGACTTCCACTGGGGCGTCCAG  
GAGGTGTGGCTGGCGGGACAGGGAGTGGTCAGCCCTGAGATGCTGCATATAAG  
CAGCTGCTTCTGCCTGTACTGGGTCTCTAGGTAGACCAGATCTGAGCCCCGGGAG

FIGURE 16

CTCTCTGGCTATCTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCCTGAGTG  
CCTTGAGTAGTGTGTGCCCGTCTGTTGTGACTCTGGTAAGAGATCCCTCAGA  
CCACTTGTGGTAGTGTGGAAAATCTCTAGCA

**FIGURE 16**

>C4\_Env\_TV1\_C\_ZA\_opt\_short (SEQ ID NO:46)

CATCACCCCTGCAGTGCAAGATCAAGCAGATCGTGCATGTGGCAGGGCGTGGCCAGGCCATGTACGCCATCG  
CCGGCAACATCACCTGC

FIGURE 17

>C4\_Env\_TV1\_C\_ZA\_opt (SEQ ID NO:47)

CTGCCCATCACCTGCAGTGCAAGATCAAGCAGATCGTGCATGTGGCAGGGCGTGGCCAGGCCATGTACCCCC  
CATGCCGGAACATCACCTGCCAGAACATCACCGCATCCTGCTGACCCGCGACGGCGGC

FIGURE 18

>C4\_Env\_TV1\_C\_ZA\_wt (SEQ ID NO:48)

TTACCCATCACACTCCAATGCAAATAAAACAAATTGTACGCATGTGGCAAGGGTAGGACAAGCAATGTATGCCCTCC  
CATTGCAGGAAACATAACATGTAGATCAAACATCACAGGAATACTATTGACACGTGATGGGGGA

FIGURE 19

>Envgp160\_TV1\_C\_ZAopt (SEQ ID NO:49)

ATGCCTGATGGCACCCAGAAGAACTGCCAGCAGTGGATCTGGGCATCCTGGCTTCTGGATGCTGATGATCTG  
CAACACCGAGGACCTGTGGGTGACCGTGTACTACGGCGTCCCCGTGGCGAGGCCAAGACCACCCCTGTTCTGCGCCA  
GCGACGCCAAGGCCAACGAGACCGAGGTGACAACGTGTGGCACCCACGCCCTGCGTGGCCACCGACCCCAACCCCCAG  
GAGATCGTGTGGCAACGTGACCGAGAACTTCAACATGTGAAAGAACACATGGCCGACCAGATGCACGAGGACATCAT  
CAGCCTGTGGACAGAGCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTGCGTACCCCTGAACCTGCACCGACACCAACG  
TGACCGCAACCGACCGTACCGGACAACACCAACGACACCAACATGCCAACGCCACCTACAAGTACGAGGAGATGAAG  
AACTGCAGCTTCAACGCCAACCGAGCTGCGGACAAGAACAGCACAAGGAGTACGCCCTGTTCTACAAGCTGGACATCGT  
GCCCTGAACGAGAACAGCAACAATTACCTACCGCTGATCAACTGCAACACACCAGCACCATACCCAGGCCCTGCC  
AGGTGAGCTTCGACCCCATCCCCATCCACTACTGCCCCCGCGACTACGCCATCCTGAAGTGAACAACAAGACCTTC  
AACGGCACCGGCCCTGCTACAACGTGAGCACCGTGCAGTGCACCCACGGCATCAAGCCGTGGTGAGCACCCAGCTGCT  
GCTGAACGGCAGCCTGGCGAGGGCATCATCCGAGCGAGAACCTGACCAGAACACCACATCGTGC  
ACCTGAACGAGAGCGTGGAGATCAACTGCACCCGCCAACAAACAACACCCGCAAGAGCGTGGCATCGGCCCCGGCAG  
GCCCTACGCCACCAACGACGTGATCGCAACATCCGCCAGGCCACTGCAACATCAGCACCGACCGCTGGACAAGAC  
CCTGCAGCAGGTGATGAAGAACGACTGGCGAGCACTCCCCAACAGACCATCAAGTTGAGCCCCACGCCGGCGAC  
TGGAGATCACCAGCAGCTCAACTGCCGGCGAGTTCTACTGCAACACCAAGAACCTGTTCAACAGCACCTAC  
TACCCCAAGAACGGCACCTACAAGTACAACGGCAACAGCAGCAGCTGCCCATCACCTGCAAGATCAAGCAGATCGT  
GCGCATGTGGCAGGGCGTGGGCAGGCCATGTACGCCCCCATGCCGCAACATCACCTGCCGAGCAACATCACCG  
GCATCTGCTGACCCCGCACGGCGCTCAACAAACCAACAAACGACACCGGAGAACCTCCGCCGGCGAC  
ATGCGGACAACACTGGCGAGCGACTGACAAGTACAAGGTGGAGATCAAGCCCTGGGATCGGCCCCACCAAGGC  
CAAGGCCCGTGGTGCAGCGAAGAACGCGCCGTGGCATCGGCCGTGTTCTGGCTTCTGGGCCGGCG  
GCACCATGGCGCCGCCAGCATCACCTGACCGTGCAGGCCAGCTGCAAGCTGGGTGGGATCGACCGCCCG  
CTGCTGAAGGCCATCGAGGCCAGCAGCACATGCTGCAAGCTGGGTGGGATCAAGCAGCTGCAGGCCCG  
GGCCATCGAGCGCTACCTGAAGGACCAAGCAGCTGGCATCTGGGATCTGGGCTGCAAGCGCCGCG  
TGCCCTGGAACAGCAGCTGGAGCAACAAAGAGCGAGGCCAGATCTGGGACAACATGACCTGGATGCAGTGGACCGCG  
ATCAACAACATACACCGAGACCATCTCCGCTGAGGACAGCCAGAACAGCAGGAGAACAGAGAACGGACCTGCT  
GGAGCTGGACAAGTGGAAACAACCTGTGGAACGGTTCGACATCAGCAACTGGCTGTTGACATCAAGATCTCATCATGA  
TCGTGGCGGCTGATCGGCTGCGCATCATCTCGCCGTGCTGAGCATCGTGAACCGCGTGCAGGCCAGGGCTACAGCCCC  
CTGAGCTTCCAGACCCCTGACCCCCAGCCCCCGGCCCTGGACCGCCTGGCGGATCGAGGAGGAGGGCGGAGCAGGA  
CCGCGACCGCAGCATCCGCCCTGGTGAGCGGCTTCTGAGGCTGGCTGGACGACTGCGCAGCCTGTGCG  
ACCACCGCCTGCCGACTTCATCTGATCGCCGTGCGGCCGTGGAGCTGCTGGGCCACAGCAGCCTGCCGGCG  
CGCGGCTGGAGATCCTGAACTGGCAGGCTGGTGAGACTGGGCTGGAGCTGAAGAACAGGCCATCAGCCC  
CCTGGACACCATGCCATGCCGTGGCGAGGGCACCGACCGCATCGAGCTGGTGAGCGCATCTGCCGCC  
TGAACATCCCCCGCGCATCCGCCAGGGCTCGAGGCCGCG  
0 10 20 30 40 50 60 70 80 90 100

FIGURE 20

>Envgp160\_TV1\_C\_ZAwT (SEQ ID NO:50)

ATGAGAGTGTGGGACACAGAAGATTGCAACAATGGTGGATATGGGCATCTTAGGCTCTGGATGCTAATGATTG  
TAACACGGAGGACTTGTGGTCACAGTCTACTATGGGTACCTGTGGAGAGAACAAAACACTCTATTCTGTGCAT  
CAGATGCTAAAGCATATGAGACAGAAGTGCATAATGCTGGCTACACATGCTGTACCCACAGACCCCAACCCACAA  
GAAATAGTTTGGAAATGTAACAGAAAATTAAATATGTGAAAAATAACATGGCAGATCAGATGCATGAGGATATAAT  
CAGTTATGGGATCAAAGCTAAAGCCATGTGTAAGTTGACCCCACTCTGTGTACTTTAAACTGTACAGATACAAATG  
TTACAGGTAATAGAACTGTACAGGTAATACAAATGATAACCAATTGCAAATGCTACATATAAGTATGAAGAAATGAAA  
AATTGCTCTTCAATGCAACCACAGAATTAAGAGATAAGAACATAAAGAGTATGACTCTTTATAAACTTGATATAGT  
ACCACTTAATGAAAATAGTAACAACTTACATATAGATTAATAAATTGCAATACCTAACCAACACAAGCCTGTCAA  
AGGTCTCTTTGACCCGATTCTACATTACTGTGCTCCAGCTGATTATGCAATTAAAGTGTAAATAAGACATTC  
AATGGGACAGGACCATGTTATAATGTCAGCACAGTACAATGTACACATGGAATTAAGCCAGTGGTATCAACTCAACT  
GTTAAATGGTAGTCTAGCAGAAGAAGGGATAATAATTAGATCTGAAAATTGACAGAGAATACAAAACAAATAATAGTAC  
ATCTTAATGAATCTGTAGAGATTAATTGACAAGGCCAACAAATAATACAAGGAAAAGTGTAAAGGATAGGACAGGACAA  
GCATTCTATGCAACAAATGACGTAATAGGAAACATAAGACAAGCACATTGTAACATTAGTACAGATAGATGGAATAAAAC  
TTTACAACAGGTAATGAAAAAAATTAGGAGAGCATTCCCTAATAAAACAAATAAAATTGACACCACATGCAGGAGGGATC  
TAGAAATTACAATGCACTGTTAATTGAGAGGAGATTTTCTATTGCAATACATCAAACCTGTTAATAGTACATAC  
TACCTTAAGAATGGTACATACAAATGGAATTCAAGCTTACACTCCATCACACTCCAATGCAAAATAAAACAAATTG  
ACGCACTGTGGCAAGGGTAGGACAAGCAATGTATGCCCTCCATTGCAGGAAACATAACATGTAGATCAAACATCACAG  
GAATACTATTGACACGTGATGGGGATTAAACAACACAAACGACACAGAGGAGACATTGACACCTGGAGGAGGAGAT  
ATGAGGGATAACTGGAGAAGTGAATTATATAAATAAAGTGGTAGAAATTAGCATTGGGATAGCACCCACTAAGGC  
AAAAAGAAGAGTGGTAGAGGAGAAAAAGAGCAGTGGGAATAGGAGCTGTGTCCTGGTCTTGGGAGCAGCAGGAA  
GCACTATGGCGCAGCGTCAATAACGCTGACGGTACAGGCCAGACAACCTGTTGCTGGTATAGTGCACAGCAAAGCAAT  
TTGCTGAAGGCTATAGAGGCGAACAGCATATGTCACACTCAGTCTGGGCTTAAGCAGCTCCAGGGAGAGTCT  
GGCTATAGAAAGATACTAAAGGATCAACAGCTCTAGGGATTGGGCTGCTGGAAAGACTCATCTGCACCACTGCTG  
TGCCTGGAACTCCAGTTGGAGTAATAATCTGAAGCAGATAATTGGGATAACATGACTGTTGATGCAGTGGGAGAGA  
ATTAATAATTACACAGAAACATAATTCAAGGTTGCTGAAAGACTCGCAAAACCCAGCAGGAAAAGAATGAAAAAGATTATT  
AGAATTGGACAAGTGGATAATCTGGAATTGGTTGACATATCAAACCTGGCTGTTGATATAAAATATTCAAATGA  
TAGTAGGAGGCTTGTAGGTTAAGAATAATTGCTGTGCTCTATAGTGAATAGAGTTAGGCAGGGACTACCTACCT  
TTGTCATTCAGACCTTACCCCAAGCCGAGGGACTCGACAGGCTGGAGGAATCGAAGAAGAAGGTGGAGAGCAAGA  
CAGAGACAGATCCATACGATTGGTGGGAGTCTGCTGCTGGACGATCTGGGAGCAGCTGCGGAGCCTGCTCTCAGCT  
ACCACCGCTTGAGAGACTTCATATTAAATTGCAAGTGAGGGCAGTGGAACTTCTGGGACACAGCAGTCTCAGGGACTACAG  
AGGGGGTGGAGATCCTTAAGTATCTGGGAGTCTGTGCACTATTGGGTCTAGAGCTAAAAAGAGTGTATTAGTCC  
GCTTGATACCATAGCAATAGCAGTAGCTGAAGGAACAGATAGGATTATAGAATTGGTACAAGAACATTGTAAGAGCTATCC  
TCAACATACCTAGGAGAATAAGACAGGGCTTGAAGCAGCTTGCTATAA

FIGURE 21

>Gag\_TV1\_C\_ZAopt (SEQ ID NO:51)

ATGGGCGCCCGGCCAGCATCCTGAGCGGGCAAGCTGGACAAGTGGAGCGCATCCGCCTCGGCCCGGGCAAGAA  
GCACTACATGCTGAAGCACCTGGTGTGGCCAGCCGAGCTGGAGCGCTCGCCCTGAACCCCGGCCCTGCTGGAGACCA  
GCGAGGGCTGCAAGCAGATCATCAAGCAGCTGCAGCCGCCCTGCAGACCGGACCGAGGAGCTGCGAGCCTGTTCAAC  
ACCGTGGCCACCTGTACTGCGTGCACAAGGGCATCGAGGTGGCGACACCAAGGAGGCCCTGGACAAGATCGAGGAGGA  
GCAGAACAAAGTGCCAGCAGAAGGCCAGCAGGCCAAGGCCCGCGACGAGAAGGTGAGCCAGAACTACCCCATCGTGAGA  
ACGCCAGGGCCAGATGGTGCACCAGGCCATCAGCCCCCGCACCTGAACGCCCTGGATCAAGGTGATCGAGGAGAACGCC  
TTCAACCCCGAGGAGATCCCCATGTTACCGGCCCTGAGCGAGGGGCCACCCCGAGGACCTGAACACCATGCTGAACAC  
CGTGGCGGCCACCAGGCCCATGCAGATGCTGAAGGACACCATCAACGAGGAGGCCGAGTGGGACCGCACCCACC  
CCGTGCACGCCGGCCCCGTGGCCCCGCCAGATGCGGAGGCCCGCGACGACATCGCCGGCACCAAGCACCCCTG  
CAGGAGCAGATGCCCTGGATGACCAGCAACCCCCCATCCCCGTGGAGGACATCTACAAGCGCTGGATCATCCTGGCCT  
GAACAAAGATCGCGCATGTACAGCCCCGTGAGCATCCTGGACATCAAGCAGGGCCCCAAGGAGGCCCTCCGCGACTACG  
TGGACCGCTTCTCAAGACCTGCGCCGAGCAGGCCACCCAGGACGTGAAGAACTGGATGACCGACACCCCTGCTGGTG  
CAAACGCCAACCCGACTGCAAGACCATCCTGCGCCCTGGCCCCGCCAGCCTGGAGGAGATGATGACCGCCTG  
CCAGGGCGTGGCGGCCAGCCACAAGGCCCGCTGCTGGCCAGGCCATGAGCCAGGCCAACAGCAACATCCTGGTGC  
AGCGCAGCAACTCAAGGGCAGCAACCGCATCATCAAGTGCCTCAACTGCGCAAGGTGGCACATGCCCGCAACTGC  
CGGCCCCCCCGCAAGAAGGGCTGCTGGAAGTGGCCAGGAGGGCCACCGAGATGAAGGACTGCACCGAGGCCAGGCCAA  
CTTCCTGGCAAGATCTGGCCAGCCACAAGGGCCGCCCGCAACTTCCGCTGAGAACCGCCCCGAGGCCACCGCCCCC  
CCGCCAGGCCACCGCCCCCGCCAGAGCTTCCGCTGAGGAGACCACCCCGTGGCCCAAGGAGAACGCCAGGCCAGTAA  
GAGCCCTGACCAGCCTGAAGAGCCTGTTCGGCAGCGACCCCTGAGCCAGTAA

FIGURE 22

>Gag\_TV1\_C\_ZAwt (SEQ ID NO:52)

ATGGGTGCGAGAGCGTCAATATTAAGCGCGGAAATTAGATAAATGGGAAAGAATTAGGTTAAGGCCAGGGGAAAGAA  
ACATTATATGTTAAAACATCTAGTATGGCAAGCAGGGAGCTGGAAAGATTGCACTTAACCTGGCCTGTTAGAAACAT  
CAGAAGGCTGTAACAAATAATAAAACAGCTACAACCAGCTTCAGACAGGAACAGAGGAACCTAGATCATTATTCAAC  
ACAGTAGCAACTCTCTATTGTGTACATAAAGGGATAGAGGTACGAGACACCAAGGAAGCCTTAGACAAGATAGAGGAAGA  
ACAAAACAAATGTCAGCAAAAGCACAACAGGCAGCTGACGAAAAGGTCAAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG  
ATGCCAAGGGAAATGGTACACCAAGCTATATCACCTAGAACATTGAATGCATGGATAAAAGTAATAGAGGAAAAGGCT  
TTCATCCAGAGGAAATACCCATGTTACAGCATTATCAGAAGGAGCCACCCCAACAGATTAAACACAATGTTAAATAC  
AGTGGGGGACATCAAGCAGCCATGCAAATGTTAAAGATACCATCAATGAGGAGGCTGCAGAATGGGATAGGACACATC  
CAGTACATGCAGGGCCTGTTGCACCAAGGCAGATGAGAGAACCAAGGGAAAGTGCACATAGCAGGAACACTACTAGTACCC  
CAGGAACAAATAGCATGGATGACAAGTAATCCACCTATTCCAGTAGAACATCTATAAAAGATGGATAATTCTGGGTT  
AAATAAAATAGTAAGAATGTATAGCCCTGTTAGCATTGGACATAAAACAAGGCCAAAAGAACCCCTTAGAGACTATG  
TAGACCGGTTCTTAAACCTTAAGAGCTGAACAAGCTACACAAGATGTTAAAGAATTGGATGACAGACACCTTGTGGTC  
CAAATGCGAACCCAGATTGTAAGACCATTAAAGAGCATTAGGACCAGGGCCTCATTAGAACATGACAGCATG  
TCAGGGAGTGGAGGACCTAGCCATAAGCAAGAGTGGCTGAGGCAATGAGCCAAGCAAACAGTAACATACTAGTGC  
AGAGAACATTAAAGGCTCTAACAGAATTAAATGTTCAACTGTGGCAAAGTAGGGCACATAGCCAGAAATTGC  
AGGGCCCTAGAAAAAGGGCTGTTGAAATGTTGACAGGAAGGACACCAATGAAAGACTGTTAGGAGGCAAGCTAA  
TTTTTAGGGAAAATTGGCCTCCCACAAGGGAGGCCAGGGAAATTCTCCAGAACAGACCAGAGCCAACAGCCCCAC  
CAGCAGAACCAACAGCCCCACCAGCAGAGAGCTCAGGTTGAGGAGACAACCCCGTGCCAGGAAGGAGAAAGAGAGG  
GAACCTTAACCTCCCTCAAATCACTCTTGGCAGCGACCCCTGTCTCAATAA

FIGURE 23

>Gag\_TV1\_ZA\_MHRopt (SEQ ID NO:53)

GACATCAAGCAGGGCCCCAAGGAGCCCTTCCCGACTACGTGGACCGCTTCAAGACC

FIGURE 24

>Gag\_TV1\_ZA\_MHRwt (SEQ ID NO:54)

GACATAAAACAAGGGCCAAAAGAACCCTTAGAGACTATGTAGACCGTTCTTAAAACC

FIGURE 25

>Nef\_TV1\_C\_ZAopt (SEQ ID NO:55)

ATGGGGGGCAAGTGGAGCAAGCGCAGCATTGGCTGGCCGTGCGAGCGCATGCGCCGACCGAGGCCGCCGC  
CGAGGGCGTGGCGCCAGGCAGGACCTGGACCGCCACGGCGCCCTGACCAGCAGCAACACCCCCGCACCAACGAGG  
CCTGCGCCTGGCTGCAGGCCAGGAGGAGGACGGCAGTGGCTTCCCCGTGCGCCCCCAGGTGCCCCCTGCGCCCCATG  
ACCTACAAGAGCGCCGTGGACCTGAGCTTCTGAAGGAGAAGGGGGCTGGAGGGCTGATCTACAGCCGCAAGCG  
CCAGGAGATCCTGGACCTGTGGGTGTACAACACCCAGGGCTTCCCCGACTGGCAGAACTACACCAGGGGGCG  
TGCCTTCCCCCTGACCTTCGGCTGGTCAAGCTGGTCCCCGTGGACCCCCGGAGGTGAAGGAGGCCAACGAGGGC  
GAGGACAACCTGCCTGCTGCACCCATGAGCCAGCGAGGACGAGGACCGCGAGGTGCTGAAGTGGAAAGTTCGA  
CAGCCTGCTGGCCCACCGCCACATGGCCCGAGCTGCACCCGAGTACTACAAGGACTGCTGA

FIGURE 26

>Nef\_TV1\_C\_ZAwT (SEQ ID NO:56)

ATGGGAGGCAAGTGGTCAAAACGCAGCATAGTTGGATGGCCTGCAGTAAGAGAAAAGAATGAGAAGAACTGAGCCAGCAGC  
AGAGGGAGTAGGAGCAGCGTCTCAAGACTTAGATAGACATGGGCACTTACAAGCAGCAACACACCTGCTACTAATGAAG  
CTTGTGCCTGGCTGCAAGCACAAGAGGAGGACGGAGATGTAGGCTTCCAGTCAGACCTCAGTACCTTAAGACCAATG  
ACTTATAAGAGTGCAGTAGATCTCAGCTTCTTTAAAAGAAAAGGGGGACTGGAAGGGTTAATTACTCTAGGAAAAG  
GCAAGAAATCCTTGATTGTGGGTCTATAACACACAAGGCTTCTCCCTGATTGGCAAAACTACACATCGGGGCCAGGG  
TCCGATTCCCACGTGACCTTGATGGTGTCAAGCTAGTACCGTTGACCCAAAGGGAGGTGAAAGAGGCCAATGAAGGA  
GAAGACAACGTGGCTACACCATGGAGCAGAGGATGAAGATAGAGAAGTATTAAAGTGGAAAGTTGA  
CAGCCTCTAGCACACAGACATGCCCGCGAGCTACATCCGGAGTATTACAAAGACTGCTGA

FIGURE 27

>NefD125G\_TV1\_C\_ZAopt (SEQ ID NO:57)

ATGGGCGGCAAGTGGAGCAAGCGCAGC ATCGTGGCTGGCCCGCGTGC GAGCGCATGC GCGCAGCGACCCGCGCGC  
CGAGGGCGTGGCGCCGCCAGGACCTGGACCGCCACGGCGCCCTGACCAGCAGCAACACCCCCGCCACCAACGGAGG  
CCTGCGCCTGGCTGCAGGCCCAGGAGGAGGACGGCGACGTGGCTTCCCGTGC GCGCCCGAGGTGCCCCCTGCGCCCCATG  
ACCTACAAGAGCGCCGTGACCTGAGCTTCTTCTGAAGGAGAAGGGCGGCTGGAGGGCCTGATCTACAGCCGCAAGCG  
CCAGGAGATCCTGGACCTGTGGGTGACAACACCCAGGGCTTCTTCCCGTGGCAGAACTACACCAGCGGCCCCGGCG  
TGCCTTCCCCCTGACCTTCGGCTGGTCTCAAGCTGGTGCCTGACCCCCCGGAGGTGAAGGAGGCCAACGAGGGC  
GAGGACAAC TGCGCTGCTGCACCCATGAGCCAGCACGGCGCGAGGACGAGGACCGCGAGGTGCTGAAGTGGAAAGTCGA  
CAGCCTGCTGGCCCACCGCCACATGGCCCGAGCTGCACCCGAGTACTACAAGGACTGCTGA

FIGURE 28

>p15RNaseH\_TV1\_C\_ZAopt (SEQ ID NO:58)

ACCTTCTACGTGGACGGGCCACCAACCGCGAGGCCAAGATCGCAAGGCCGGCTACGTGACCGACCGCGGCCAGAA  
GATCGTGACCTGACCAACACCACCAACCAGAAGACCGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGGCAGCG  
AGGTGAACATCGTGAACGACAGCCAGTACGCCCTGGGCATCATCCAGGCCAGCCGACAAGAGCGACAGCGAGATCTTC  
AACCAGATCATCGAGCAGCTGATCAACAAGGAGCGCATCTACCTGAGCTGGGTGCCGCCACAAGGGCATCGCGCAA  
CGAGCAGGTGGACAAGCTGGTGAGCAAGGGCATC

FIGURE 29

>p15RNaseH\_TV1\_C\_Zawt (SEQ ID NO:59)

ACTTTCTATGTAGATGGAGCAACTAATAGGAAAGCTAAAATAGGAAAAGCAGGGTATGTTACTGACAGAGGAAGGCAGAA  
AATTGTTACTCTAACTAACACAACAAATCAGAAGACTGAGTTACAAGCAATTCAAGCTAGCTCTGCAGGATTCAAGGATCAG  
AAGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCATTCAAGCACAACCAGATAAGAGTGACTCAGAGATATT  
AACCAAATAATAGAACAGTTAATAAACAAAGGAAAGAATCTACCTGTATGGGTACCAGCACATAAGGAATTGGGGAAA  
TGAACAAGTAGATAAATTAGTAAGTAAGGAAATT

FIGURE 30

>p31Int\_TV1\_C\_Zaopt (SEQ ID NO:60)

CGCAAGGTGCTGTTCTGGACGGCATCGACAAGGCCAGGAGGAGCACGAGCGTACACAGCAACTGGCGGCCATGGC  
CAACGAGTTCAACCTGCCCCCCTCGTGGCAAGGAGATCGTGGCAGCTGCGACAAGTGCAGCTGAAGGGCGAGGCCA  
TCCACGGCCAGGTGGACTGCAGCCCCGGCATCTGGCAGCTGGACTGCACCCACCTGGAGGGCAAGATCATCCTGGC  
GTGCACGTGGCCAGCGCTACATGGAGGCCAGGTGATCCCCGCCAGACCGCCAGGAGACCGCCTACTTCATCCTGAA  
GCTGGCCGGCGCTGGCCGTGAAGGTGATCCACACCGACAACGGCAGCAACTTCACCAGCACCGCCGTGAAGGCC  
GCTGGTGGCCGGCATCCAGCAGGAGTTGGCATCCCTACAACCCAGAGCCAGGGCGTGGTGGAGAGCATGAACAAG  
GAGCTGAAGAACAGATCATGGCCAGGTGCGCAGCAGGCCAGGCGACCTGAAGACCGCCGTGAGATGGCCGTGTTATCCA  
CAACTTCAAGCGCAAGGGCGCATCGCGCTACAGCGCCGGCAGCGCATCATCGACATCATGCCACCGACATCCAGA  
CCAAGGAGCTGCAGAACAGATCATCCGATCCAGAACCTCCGCGTGTACTACCGCGACAGCCGCGACCCATCTGAAG  
GGCCCCCGCCGAGCTGCTGTGGAAGGGCGAGGGCGTGGTGTGAGGACAAGGGCGACATCAAGGTGGTGGCCCG  
CAAGGCCAAGATCATCCGCACTACGGCAAGCAGATGGCCGGCGCCACTGCGTGGCCGGCCAGGACGAGGAAC

FIGURE 31

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DOI: 10.1098/rspa.2003.1000  
Published online 20 January 2004  
in J. R. Soc., Interface  
http://rsta.royalsocietypublishing.org

>p31Int\_TV1\_C\_ZAwT (SEQ ID NO:61)

AGGAAAGTGGTGTCTAGATGGAATAGATAAAGCTCAAGAAGAGCATGAAAGGTACACAGCAATTGGAGAGCAATGGC  
TAATGAGTTAATCTGCCACCCATAGTAGCAAAGAAATAGTAGCTGTGATAATGTCAGCTAAAAGGGGAAGCCA  
TACATGGACAAGTCGACTGTAGTCAGGGATATGGCAATTAGATTGTACCCATTAGAGGGAAAATCATCCTGGTAGCA  
GTCCATGTAGCTAGTGGCTACATGGAAGCAGAGGTTATCCAGCAGAAACAGGACAAGAACAGCATATTTATATTTAA  
ATTAGCAGGAAGATGGCAGTCAGTAATACATACAGACAATGGCAGTAATTTACCACTGAGCTTAAGGCAGCCT  
GTGGTGGCAGGTATCCAACAGGAATTGGAATTCCCTACAATCCCCAAAGTCAGGGAGTGGTAGAATCCATGAATAAA  
GAATTAAAGAAAATAATAGGACAAGTAAGAGATCAAGCTGAGCACCTAACAGCAGTACAAATGGCAGTATTCAATTCA  
CAATTTAAAAGAAAAGGGGAATTGGGGGGTACAGTGCAGGGAAAGAATAATAGACATAATAGCAACAGACATACAAA  
CTAAAGAATTACAAAACAATTATAAGAATTCAAATTTCGGGTTATTACAGAGACAGCAGAGACCCATTGGAAA  
GGACCAGCCGAACTACTCTGGAAAGGTGAAGGGTAGTAGTAATAGAAGATAAAGGTGACATAAAGGTAGTACCAAGGAG  
GAAAGCAAAATCATTAGAGATTATGGAAAACAGATGGCAGTGCTGATTGTGGCAGGTGGACAGGATGAAGAT

FIGURE 32

>Pol\_TV1\_C\_ZAopt (SEQ ID NO:62)

TTCTTCCGCAGAACCTGGCTTCCCCAGGGCGAGGCCCGAGTTCCCCCGAGCAGACCCGCACAGCCCCAC  
CAGCCGCACCAACAGCCCCACCAGCCCGAGCTGCAGGTGCGCGCGACAACCCCGCGCCAGGAGGGCGAGCGCGAGG  
GCACCTTCAACTCCCCAGATCACCTGTGGCAGCGCCCCCTGGTAGAGCATCAAGGTGGAGGGCCAGATCAAGGAGGC  
CTGCTGGACACCGCGCCGACGACCCGTGCTGGAGGAGATCGACCTGCCCAGCAAGTGGAGGCCAGATGATCGCG  
CATCGCGGCTTCATCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTGCGCAAGAAGGCCATCGCACCGTGC  
TGGGGCCCCACCCCCGTGAACATCATCGGCCAACCTGCTGACCCAGCTGGCTGCACCCCTGAACCTCCCCATCAGC  
CCCATCGAGACCCTGCCCCGTGAAGCTGAAGGCCGCATGGACGCCCAAGGTGAAGCAGTGGCCCCCTGACCGAGGAGAA  
GATCAAGGCCCTGACCCGCATCTCGAGGAGATGGAGAAGGGAGGGCAAGATCACCAAGATCGGCCGCACAACCCCTACA  
ACACCCCGTGTGCGCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGACTTCCGCGAGCTGAACAAGCGC  
ACCCAGGACTCTGGGAGGTGCAGCTGGCATTCCCCCACCCCGCCCTGAAGAAGAAGAAGAGCGTGAACCGTGC  
CGTGGCGACGCCACTCTCAGCGTCCCCCTGGACGAGAGCTCCGCAAGTACACGCCCTCACCATCCCCAGCATCAACA  
ACGAGACCCCCGGCATCCGCTACCAGTACAACGTGCTGCCCAAGGCTGGAGGGCAGGCCCATCTTCCAGAGCAGC  
ATGACCAAGATCTGGGCCCTTCCGCGCAAGAACCCGACATCGTATCTACAGTACATGGACGACCTGTACGTGG  
CAGCGACCTGGAGATCGGCCAGCACCGCGCAAGATCGAGGAGCTGCGCGAGCACCTGCTGAAGTGGGCTTCACCACCC  
CCGACAAGAACGACCAAGGAGCCCCCTCTGTGGATGGCTACGAGCTGCAACCCGACAAGTGGACCGTGCAGGCC  
ATCCTGCTGCCGAGAACGGACAGCTGGACCGTGAACGACATCCAGAACGCTGGCAAGCTGAACCTGGGCCAGCAGAT  
CTACCCCGGCATCAAGGTGCGCCAGCTGTGCAAGCTGCGCGCCAGGCCATCGTGCACGGCTGTACTACGACCCAGCAAG  
GACCTGATGCCGAGATCCAGAACGAGGCCACGAGCAGTGGACCTACAGATCTACCAAGGAGCCCTCAAGAACCTGAA  
GACCGCAAGTACGCCAAGATCGCACCAACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAACGATGCCA  
TGGAGAGCATCGTATCTGGGCAAGACCCCCAAGTTCCGCTGCCATCCAGAACGGAGACCTGGAGACCTGGTGGACC  
GACTACTGGCAGGCCACCTGGATCCCCAGTGGAGTGGAGTTCGTGAACACCCCCCTGGTAGAGCTGTGGTACAGCTGGA  
GAAGGACCCCATCGCCGGCGTGGAGACCTTCTACGTGGACGGCGCCACCAACCGCAGGCCAGATCGCAAGGCCGGCT  
ACGTGACCGACCGCGGCCAGAACGATCGTACCCCTGACCAACACCAACCGAGCTGAGGCCATCCAG  
CTGGCCCTGAGGACAGCGCAGCGAGGTGAACATCGTACCGACAGCCAGTACGCCCTGGCATCATCCAGGCCAGCC  
CGACAAGAGCGACAGCGAGATCTCAACCAGATCATCGAGCAGCTGATCAACAAGGAGCGCATCTACCTGAGCTGGTGC  
CCGCCACAAGGGCATCGCCGGCAACGAGCAGGTGGACAAGCTGGTAGCAAGGGCATCCGAAGGTGCTTCCCTGGAC  
GGCATCGACAAGGCCAGGGAGGAGCACGAGCGCTACCAACAGCAACTGGCGCCATGGCAACGAGTTCAACCTGCC  
CATCGTGGCCAAGGAGATCGTGGCCAGCTGCGACAAGTGCCAGCTGAAGGGCGAGGCCATCCACGGCCAGGTGGACTGCA  
GCCCGGCATCTGGCAGCTGGACTGACCCACCTGGAGGGCAAGATCATCCTGGTGGCCGTGCACGTGGCCAGCGGC  
ATGGGAGGCCGAGGTGATCCCCGCCAGACCGGCCAGGAGACCGCTACTTCATCTGAAGCTGGCCGGCGCTGGCC  
GAAGGTGATCCACACCCGACAACGGCAGCAACTCACCAGCACCGCCCTGAAGGGCGCTGCTGGTGGCCGATCCAGC  
AGGAGTTCGGCATCCCCATCAACCCCCAGAGCCAGGGCGTGGTAGAGCATGAACAAGGAGCTGAAGAACGATCATCGC  
CAGGTGCGCAGGCCAGGCGAGCACCTGAAGACCGCCGTGCAGATGGCCGTGTTCATCCACAACCTCAAGCGCAAGGGCG  
CATCGCGGCTACAGCGCCGGCGAGCGCATCATCGACATCATGCCACCGACATCCAGAACGAGCTGCAGAACAGA  
TCATCCGCATCCAGAACCTCCGCGTACTACCGCAGGCCAGGGCCATCTGAAGGGCCCGAGCTGCTGTGG  
AAGGGCGAGGGCGTGGTGGTAGCGAGGACAAGGGCGACATCAAGGTGGTCCCCGCCAGGACGAGGAC  
CTACGGCAAGCAGATGGCCGGCGCCACTGCGTGGCCGGCGCCAGGACGAGGAC

FIGURE 33

>Pol\_TV1\_C\_ZAwT (SEQ ID NO:63)

TTTTTTAGGGAAAATTGGCCTTCCCACAAGGGGAGGCCAGGAATTCCCTCCAGAACAGACCAGAGCCAACAGCCCCAC  
CAGCAGAACCAACAGCCCCACCAGCAGAGAGCTTCAGGTTGAGGAGACAACCCCGTGCCAGGAAGGAGAAAGAGAGG  
GAACCTTTAACCTCCCTCAAATCACTCTTGGCAGCGACCCCTGTCTCAATAAAAGTAGAGGGCCAGATAAAGGAGGCT  
CTCTTAGACACAGGAGCAGATGATACAGTATTAGAAGAAATAGATTGCCAGGGAAATGAAACCAAAATGATAGGGGG  
AATTGGAGGTTTATCAAAGTAAGACAGTATGATCAAATACTTATAGAAATTGTGGAAAAAAGGCTATAGGTACAGTAT  
TAGTAGGGCCTACACCAAGTCAACATAATTGGAAGAAATCTGTTACTCAGCTTGGATGCACACTAAATTTCCTAATTAGT  
CCTATTGAAACTGTACCAAGTAAATTAAAACCAGGAATGGATGCCAAAGGTCAAACAATGCCATTGACAGAAGAAAA  
AATAAAAGCATTAACAGAATTGTGAGGAATGGAGAAGGAAAGGAAATTACAAAATTGGCCTGATAATCCATATA  
ACACTCCAGTATTGCCATAAAAAGAAGGACAGTACTAAGTGGAGAAAATTAGTAGATTTCAGGGAACTCAATAAAGA  
ACTCAAGACTTTGGAGTTCAATTAGGAATACACACCCAGCAGGATTAAAAAGAAAAATCAGTGAAGTGTAGA  
TGTGGGGGATGCATATTTCAGTCTTGTAGATGAAAGCTTCAGGAAATATACTGCATTCAACCATACCTAGTATAAAC  
ATGAAACACCAGGGATTAGATATCAATATACTGCTGCCACAGGGATGGAAAGGATCACAGCAATATTCCAGAGTAGC  
ATGACAAAAATCTTAGAGGCCCTTCAGAGCAAAAATCCAGACATAGTTATCTATCAATATGGATGACTTGTATGTAGG  
ATCTGACTTAGAAATAGGGCAACATAGAGCAAAAATAGAAGGTTAAGGAAACATTATTGAAATGGGATTACAACAC  
CAGACAAGAACATCAAAAAGAACCCCCATTCTTGGATGGGTATGAACTCCATCCTGACAAATGGACAGTACAACCT  
ATACTGCTGCCAGAAAAGGATAGTGGACTGTCATGATATACTGAAAGTTAGTGGAAAATTAAACTGGCAAGTCAGAT  
TTACCCAGGGATTAAAGTAAGGCAACTCTGTAACACTCCTCAGGGGGCCAAAGCCTAACAGACATAGTACCAACTG  
AAGAAGCAGAATTAGAATTGGCAGAGAACAGGGAAATTAAAGAGAACAGTACATGGAGTATATTGATCCATCAAAA  
GACTTGATAGCTGAAATACAGAACAGGGGCATGAACTGGACATATCAAATTATCAAGAACCAATTAAAGTCTGAA  
AACAGGGAAAGTATGCAAAAATGAGGACTACCCACACTAATGATGTAACAGAGGCACTGCAAAAATAGCCA  
TGAAAGCATAGTAATATGGGAAAGACTCCTAAATTAGACTACCCATCCAAAAGAAACATGGAGACATGGTGGACA  
GACTATTGGAAGCCACCTGGATCCCTGAGTGGAGTTGTTAATACCCCTCCCTAGTAAATTATGGTACCAACTAGA  
AAAAGATCCCCTAGCAGGAGTAGAAACTTCTATGTAGATGGAGCAACTAATAGGAAAGCTAAATAGGAAAGCAGGGT  
ATGTTACTGACAGAGGAAGGAGAAAATTGTTACTCTAACTACACAACAAATCAGAAGACTGAGTTACAAGCAATTCA  
CTAGCTCTGCAGGATTCAAGGATCAGAAGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCTCAAGCACA  
AGATAAGAGTGAACAGAGATATTAAACAAATAAGAACAGTTAAATAACAAGGAAAGAATCTACCTGTATGGTAC  
CAGCACATAAGGAATTGGGAAATGAAACAGTAGATAATTAGTAAGTAAGGAAATTAGGAAAGTGTGTTCTAGAT  
GGAATAGATAAAAGCTCAAGAAGAGCATGAAAGGTACCAACAGCAATTGGAGAGCAATGGCTAATGAGTTAATCTGCCACC  
CATAGTAGAAAAGAAATAGTAGCTGTGATAATGTCAGCTAAAAGGGGAAGCCATACATGGACAAGTCGACTGTA  
GTCCAGGGATATGGAATTAGATTGTAACCATTTAGAGGGAAAATCATCCTGGTAGCAGTCCATGTAAGCTAGTGGCTAC  
ATGGAAGCAGAGGTTATCCCTAGCAGAACAGGACAAGAACAGCATATTATTTATATTAAATTAGCAGGAAGATGGCAGT  
CAAAGTAATACATACAGACAATGGCAGTAATTTCACAGTACTGCAGTTAAGGAGCCTGTTGGCAGGTATCCAAC  
AGGAATTGGAAATTCCCTACAATCCCCAAAGTCAGGGAGTGGTAGAATCCATGAATAAGAATTAAAGAAAATAATAGGA  
CAAGTAAGAGATCAAGCTGAGCACCTTAAGACAGCAGTACAATGGCAGTATTCACTACAAATTAAAGAAAAGGGGG  
AATTGGGGGTACAGTGCAGGGAAAGAATAATAGACATAATAGCAACAGACATACAAACTAAAGAATTACAAAAACAAA  
TTATAAGAATTCAAATTTCGGTTTATTACAGAGACAGCAGAGACCCATTGGAAGGACCAGCCGAACTACTCTGG  
AAAGGTGAAGGGTAGTAGTAATAGAAGATAAAGGTGACATAAAGGTAGTACCAAGGAGGAAAGCAAAATCATTAGAGA  
TTATGGAACAGATGGCAGGTGCTGATTGTGGCAGGTGGACAGGATGAAGAT

FIGURE 34

>Prot\_TV1\_C\_ZAopt (SEQ ID NO:64)

CCCCAGATCACCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGAGGGCCAGATCAAGGAGGCCCTGCTGGACACCGG  
CGCCGACGACACCGTGCTGGAGGAGATCGACCTGCCCGCAAGTGGAAAGCCCAAGATGATCGGCGGCATCGGCGGCTTCA  
TCAAGGTGCCAGTACGACCAGATCCTGATCGAGATCTGCCAGAAGAAGGCCATCGGCACCGTGCTGGTGGCCCCACC  
CCCGTGAACATCATCGGCCAACCTGCTGACCCAGCTGGCTGCACCCCTGAACCTC

FIGURE 35

>Prot\_TV1\_C\_ZAwt (SEQ ID NO:65)

CCTCAAATCACTTTGGCAGCGACCCCTGTCTCAATAAAAGTAGAGGGCCAGATAAAGGAGGCTCTTAGACACAGG  
AGCAGATGATACAGTATTAGAAGAAATAGATTGCCAGGAAATGGAAACCAAAATGATAGGGGAATTGGAGGTTTA  
TCAAAGTAAGACAGTATGATCAAATACTTATAGAAATTGTGGAAAAAAGGCTATAGGTACAGTATTAGTAGGGCCTACA  
CCAGTCAACATAATTGGAAGAAACTGTTAAGCTAGCTGGATGCACACTAAATT

FIGURE 36

>Protina\_TV1\_C\_ZAopt (SEQ ID NO:66)

CCCCAGATCACCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGAGGGCCAGATCAAGGAGGCCCTGCTGGCCACCGG  
CGCCGACGACACCGTGCTGGAGGAGATCGACCTGCCCGCAAGTGGAAAGCCAAGATGATCGCGGCATCGCGGCTTCA  
TCAAGGTGCCAGTACGACCAGATCCTGATCGAGATCTGCGGCAAGAAAGGCCATCGGCACCGTGCTGGTGGCCCCACC  
CCCGTGAACATCATCGGCCGCAACCTGCTGACCCAGCTGGCTGCACCCCTGAACCTC

FIGURE 37

>Protina\_TV1\_C\_ZAwT (SEQ ID NO:67)

CCTCAAATCACTTTGGCAGCGACCCCTTGTCTCAATAAAAGTAGAGGGCCAGATAAAGGAGGCCTCTTAGCCACAGG  
AGCAGATGATACTAGTATTAGAAGAAATAGATTTGCCAGGAAATGGAACCCAAAATGATAGGGGAATTGGAGGTTTA  
TCAAAGTAAGACAGTATGATCAAATACTTATAGAAATTGTGGAAAAAAGGCTATAGGTACAGTATTAGTAGGGCCTACA  
CCAGTCAACATAATTGGAAGAAATCTGTTAACTCAGCTTGGATGCACACTAAATT

FIGURE 38

Both the *labeled* and *unlabeled* data sets were used to train the model, and the results are shown in Table 1.

>ProtinaRTmut\_TV1\_C\_ZAopt (SEQ ID NO:68)

CCCCAGATCACCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGAGGGCCAGATCAAGGAGGCCCTGCTGGCCACCGG  
CGCCGACGACACCGTGCCTGGAGGAGATCGACCTGCCGGCAAGTGGAAAGCCAAGATGATCGCGGCATCGCGGCTTCA  
TCAAGGTGCGCCAGTACGACCAGATCCTGATCGAGATCTCGGGCAAGAAGGCCATCGGCACCGTGCCTGGGGCCCCACC  
CCCGTGAACATCATCGGCCGCAACCTGCTGACCCAGCTGGCCTGCACCCCTGAACCTCCCCATCAGCCCCATCGAGACCGT  
GCCCGTGAAGCTGAAGCCGGCATGGACGGCCCCAAGGTGAAGCAGTGGCCCTGACCGAGGAGAAGATCAAGGCCCTGA  
CCGCCATCTCGGAGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCGACAACCCCTACAACACCCCCGTGTT  
GCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGGACTTCCGCGAGCTGAACAAGCGCACCCAGGACTTCTG  
GGAGGTGCAGCTGGCATCCCCCACCCGCCGGCTGAAGAAGAAGAGCGTGACCGTGCCTGGACGTGGCGACGCC  
ACTTCAGCGTGCCTGGACGAGAGCTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAACAACGAGACCCCCGGC  
ATCCGCTACCAGTACAACGTGCTGCCCAAGGGCTGGAAGGGCAGCCCCCCTATCTCCAGAGCAGCATGA<sup>C</sup>CAAGATCCT  
GGAGCCCTTCCGCCAAGAACCCCCGACATCGTGTACTACCAGGCCCTGTACGTGGGAGCGACCTGGAGATCGGC  
AGCACCGCGCCAAGATCGAGGAGCTCGCGAGCACCTGCTGAAGTGGGCTTCACCAACCCCGACAAGAACCGAGAAC  
GAGCCCCCCTTCTGCCCCATCGAGCTGCACCCGACAAGTGGACCGTGCAGCCCATCCTGCTGCCGAGAACGGACAGCTG  
GACCGTGAACGACATCCAGAAGCTGGTGGCAAGCTGAACTGGCCAGCCAGATCTACCCGGCATCAAGGTGCGCCAGC  
TGTGCAAGCTGCTGCGGCCAAGGCCCTGACCGACATCGGCCCTGACCGAGGAGGCCAGCTGGAGCTGGCGAG  
AACCGCGAGATCTGCGCGAGCCCGTGCACGGCGTGTACTACGACCCAGCAAGGACCTGATCGCGAGATCCAGAAC  
GGGCCACGAGCAGTGGACTTACAGATCTACCGAGGCCCTCAAGAACCTGAAGAACCGGCAAGTACGCCAGATGCG  
CCACCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGAGAACGATCGCCATGGAGAGCAGTGTGACTGGGCAAG  
ACCCCCAAGTCCGCTGCCATCCAGAACGGAGACCTGGAGACCTGGTGGACCGACTACTGGCAGGCCACCTGGATCCC  
CGAGTGGAGTCGTGAACACCCCCCCCCCTGGTGAAGCTGTGGTACCAAGCTGGAGAACGGACCCATGCCGGCGTGGAGA  
CCTTCTACGTGGACGGGCCACCAACCGCGAGGCCAGATCGGCAAGGCCGGCTACGTGACCGACCGCGGCCAGAAC  
ATCGTACCCCTGACCAACACCACCAACCAGAACGAGCTGCAGGCCATCCAGCTGGCCCTGCAGGACAGCGAGCGA  
GGTGAACATCGTGGACCGACAGCCAGTACGCCCTGGCATCATCCAGGCCAGGCCAGAACAGAGCGACAGCGAGATCTCA  
ACCAAGATCATCGAGCAGCTGATCAACAAGGAGCGCATCTACCTGAGCTGGGTGCCGCCACAAGGGCATCGCGGCCAAC  
GAGCAGGTGGACAAGCTGGTGGAGCAAGGGCATCCGCAAGGTGCTG

FIGURE 39

>ProtinaRTmut\_TV1\_C\_ZAwT (SEQ ID NO:69)

CCTCAAATCACTCTTGGCAGCGACCCCTGTCCTCAATAAAAGTAGAGGGCCAGATAAAGGAGGCTCTTAGCCACAGG  
AGCAGATGATACTAGTATTAGAAGAAATAGATTGCCAGGGAAATGGAAACCAAAATGATAGGGGAATTGGAGGTTTA  
TCAAAGTAAGACAGTATGATCAAATACTTATAGAAATTGTGAAAAAAGGCTATAGGTACAGTATTAGTAGGGCCTACA  
CCAGTCACATAATTGGAAGAAATCTGTTAECTCAGCTTGATGCACACTAAATTCCAATTAGTCCTATTGAAACTGT  
ACCAGTAAAATTAAAACCAGGAATGGATGCCAAAGGTCAAACAATGCCATTGACAGAAGAAAAATAAAAGCATTAA  
CAGCAATTGTGAGGAAATGGAGAAGGAAAGGAAAAATTACAAAATTGGCCTGATAATCCATATAACACTCCAGTATTT  
GCCATAAAAAGAAGGACAGTACTAAGTGGAGAAAATTAGTAGATTCAGGGACTCAATAAAAGAACTCAAGACTTTG  
GGAAGTTCAATTAGGAATACCACACCCAGCAGGATTAAAAAGAAAAATCAGTGACAGTGCTAGATGTGGGGATGCAT  
ATTTCAGTTCTTTAGATGAAAGCTTCAGGAAATATACTGCATTCACTACCTAGTATAAACATGAAACACCAGGG  
ATTAGATATCAATATAATGTGCTGCCACAGGGATGAAAGGATCACCAGCAATATTCCAGAGTAGCATGA~~A~~AAAATCTT  
AGAGCCCTTCAGAGCAAAAATCCAGACATAGTTATCTATCAAGCCCCGTTGATGTAGGATCTGACTTAGAAATAGGGC  
AACATAGAGCAAAAATAGAAGAGTTAGGGAACATTATTGAAATGGGATTACACACCAGACAAGAAACATCAAAAA  
GAACCCCCATTCTTCCCATCGAACTCCATCCTGACAATGGACAGTACAACCTATACTGCTGCCAGAAAGGATAGTTG  
GACTGTCAATGATATACAGAAGTTAGTGGAAAATTAACTGGCAAGTCAGATTACCCAGGGATTAAAGTAAGGCAAC  
TCTGAAACTCCTCAGGGGGCCAAAGCACTAACAGACATAGTACCAACTGAAGAAGCAGAATTAGAATTGGCAGAG  
AACAGGGAAATTAAAGAGAACAGTACATGGAGTATTATGATCCATCAAAGACTTGATAGCTGAAATACAGAAACA  
GGGGCATGAACAATGGACATATCAAATTATCAAGAACCATTTAAAATCTGAAAACAGGGAGTATGCCAAAATGAGGA  
CTACCCACACTAATGATGTAAAACAGTTAACAGAGGCACTAACAGACATAGTACCAACTGAAGAAGCAGAATTAGAATTGGCAGAG  
ACTCCTAAATTAGACTACCCATCCAAAAGAACATGGAGACATGGTGGACAGACTATTGCAAGCCACCTGGATCCC  
TGAGTGGAGTTGTTAATACCCCTCCCTAGTAAAATTATGGTACCAACTAGAAAAGATCCCATAGCAGGAGTAGAAA  
CTTTCTATGTAGATGGAGCAACTAATAGGGAGCTAAAATAGGAAAGCAGGGTATGTTACTGACAGAGGAAGGCAAGAAA  
ATTGTTACTCTAACTAACACAACAAATCAGAAGACTGAGTTACAAGCAATTCTAGCTGCAAGGATTCTAGGATCAGA  
AGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCTACCTGTATGGTACCCAGCACATAAGGAATTGGGGAAAT  
ACCAAATAATAGAACAGTTAACACAAGGAAAGAATCTACCTGTATGGTACCCAGCACATAAGGAATTGGGGAAAT  
GAACAAGTAGATAATTAGTAAGGAATTAGGAAAGTGTG

FIGURE 40

>ProtwtRTwt\_TV1\_C\_ZAopt (SEQ ID NO:70)

CCCCAGATCACCTGTGGCAGCGCCCCCTGGTGAGCATCAAGGTGGAGGGCCAGATCAAGGAGGCCCTGCTGGACACCGG  
CGCCGACGACCCGTGCTGGAGGAGATCGACCTGCCGGCAAGTGGAGGCCAAGATGATCGCGGCATCGGCCGCTTC  
TCAAGGTGCGCAGTACGACCAGATCCTGATCGAGATCTCGGGCAAGAAGGCCATCGCACCGTCTGGTGGGCCACC  
CCCGTGAACATCATCGGCCGCAACCTGCTGACCCAGCTGGCTGCACCCCTGAACCTCCCCATCGACCCATCGAGACCGT  
GCCCGTGAAGCTGAAGCCGGCATGGACGGCCCCAAGGTGAAGCAGTGGCCCTGACCGAGGAGAAGATCAAGGCCCTGA  
CCGCATCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACAAGATCGGCCGACAACCCCTACAACACCCCCGTGTT  
GCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACTTCGCGAGCTGAACAAGCGCACCCAGGACTTCTG  
GGAGGTGCAGCTGGCATCCCCACCCGCCGGCTGAAGAAGAAGAAGAGCGTGAACGTGCTGGACGTGGCGACGCC  
ACTTCAGCGTGCCCTGGACGAGAGCTTCCGCAAGTACACCGCCTTCACCATCCCCAGCATCAACAACGAGACCCCCGGC  
ATCCGCTACCACTGCTGCCCAAGGGCTGGAAGGGCAGCCCATCTCCAGAGCAGCATGA CAAGATCCT  
GGAGCCCTCCGCCAAGAACCCGACATCGTGTACCATCAGTACATGGACGACTGTACGTGGCGACCTGGAGA  
TCGGCCAGCACCAGCAAGATCGAGGAGCTGGCGAGCACCTGCTGAAGTGGGCTTCACCAACCCCCGACAAGAAC  
CAGAAGGAGCCCCCTTCTGTGGATGGCTACGAGCTGACCCGACAAGTGGACCGTGCAGCCCCTGCTGCCGA  
GAAGGACAGCTGGACCGTGAACGACATCCAGAAGCTGGTGGCAAGCTGAACCTGGCCAGCAGATCTACCCGGCATCA  
AGGTGCGCCAGCTGTGCAAGCTGCTGGCGGCCAAGGCCCTGACCGACATCGTGCCTGACCGAGGAGGCCAGCTG  
GAGCTGGCGAGAACCGCAGATCCTGCGAGGCCCTGACGGCGTACTACGACCCAGCAAGGACCTGATCGCCGA  
GATCCAGAAGCAGGCCACGAGCAGTGGACCTACCAAGATCTACCAAGGAGCCCTCAAGAACCTGAAGACCGGCAAGTACG  
CCAAGATGCGCACCAACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAAGATGCCATGGAGAGCATCGT  
ATCTGGGCAAGACCCCCAAGTTCCGCTGCCATCCAGAAGGAGACCTGGAGACCTGGTGGACTACTGGCAGG  
CACCTGGATCCCCGAGTGGAGTTGGTAACACCCCCCCCCCTGGTGAAGCTGTTACAGCTGGAGAAGGACCCATCG  
CCGGCGTGGAGACCTTCTACGTGGACGGGCCACCAACCGCAGGCCAAGATCGGCAAGGCCGCTACGTGACCGACCG  
GGCCGCCAGAAGATCGTGACCCCTGACCAACACCACCAACCAGAAGACCGAGCTGACGCCATCCAGCTGCCCTGCGAGA  
CAGCGGCAGCGAGGTGAACATCGTGACCGACGCCAGTACGCCCTGGCATCATCCAGGCCAGGCCACAAGAGCGACA  
GCGAGATCTTCAACCAGATCATCGAGCAGCTGATCAACAAGGAGCGCATCTACCTGAGCTGGTGGCCGCCACAAGGGC  
ATCGGCGGCAACGAGCAGGTGGACAAGCTGGTGGAGCAAGGGCATCCGCAAGGTGCTG

FIGURE 41

>ProtwtRTwt\_TV1\_C\_ZAw (SEQ ID NO:71)

CCTCAAATCACTCTTGGCAGCGACCCCTTGTCTCAATAAAAGTAGAGGGCCAGATAAAGGAGGCTCTCTTAGACACAGG  
AGCAGATGATACTAGTATTAGAAGAAATAGATTGCCAGGAAATGAAACCAAAATGATAGGGGATTGGAGGTTTA  
TCAAAGTAAGACAGTATGATCAAATACTTATAGAAATTGTGAAAAAAGGCTATAGGTACAGTATTAGTAGGGCCTACA  
CCAGTCACATAATTGAAAGAAATCTGTTACTCAGCTTGATGCACACTAAATTCCAATTAGTCCTATTGAAACTGT  
ACCAGTAAAATAAAACCAGGAATGGATGCCAAAGGTCAAACAATGCCATTGACAGAAGAAAAATAAAAGCATTAA  
CAGCAATTGTGAGGAAATGGAGAAGGAAGGAAAATTACAAAATTGGGCCTGATAATCCATATAACACTCCAGTATT  
GCCATAAAAAGAAGGACAGTACTAAGTGGAGAAAATTAGTAGATTCAGGGACTCAATAAAAGAACTCAAGACTTTG  
GGAAGTTCAATTAGGAATACCACACCCAGCAGGATTAAAAAGAAAAATCAGTGACAGTGCTAGATGTGGGGATGCAT  
ATTTCAGTCCCTTAGATGAAAGCTTCAGGAAATATACTGCATTCAACCATACCTAGTATAAAACAATGAAACACCAGGG  
ATTAGATATCAATATAATGTGCTGCCACAGGGATGAAAGGATCACCAGCAATATCCAGAGTAGCATGA~~A~~AAAATCTT  
AGAGCCCTTCAGACAAAAATCCAGACATAGTTATCTAATATATGGATGACTTGTATGTAGGATCTGACTTAGAAA  
TAGGGCAACATAGACAAAAATAGAAGAGTTAGGGAAACATTATTGAAATGGGATTACACACCAGACAAGAAACAT  
CAAAAAGAACCCCCATTCTTGGATGGGTATGAACTCCATCTGACAAATGGACAGTACAACCTATACTGCTGCCAGA  
AAAGGATAGTGGACTGTCATGATATAACAGAAGTTAGTGGAAAATTAAACTGGCAAGTCAGATTACCCAGGGATTA  
AAGTAAGGCAACTCTGAACTCCTCAGGGGGCCAAAGCACTAACAGACATAGTACCAACTAATGAAAGCAGAATT  
GAATTGGCAGAGAACAGGGAAATTTAAGAGAACAGTACATGGAGTTATTGATCCATCAAAGACTTGATAGCTGA  
AATACAGAAACAGGGCATGAAACATGGACATATCAAATTATCAAGAACCAATTAAACTCTGAAAACAGGGAGTATG  
CAAAAATGAGGACTACCCACACTAATGATGTAACAGAGGCAGTGCAAAAATAGCCATGGAAAGCATACTGA  
ATATGGGAAAGACTCCTAAATTAGACTACCCATCCAAAAGAAACATGGAGACATGGTGGACAGACTATTGGCAAGC  
CACCTGGATCCCTGAGTGGAGTTGTTAATACCCCTCCCTAGTAAAATTATGGTACCAACTAGAAAAAGATCCCTAG  
CAGGAGTAGAAACTTTCTATGTAGATGGAGCAACTAATAGGGAAAGCTAAATAGGAAAGCAGGGTATGTTACTGACAGA  
GGAAGGCAGAAAATTGTTACTCTAACTAACACAACAAATCAGAAGACTGAGTTACAAGCAATTCTAGCTCTGCAGGA  
TTCAGGATCAGAACTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCTCAAGCACAACCAGATAAGAGTGA  
CAGAGATATTAAACAAATAATAGAACAGTTAATAAACAAGGAAAGAATCTACCTGTCATGGTACCGACACATAAGGA  
ATTGGGGAAATGAACAGTAGATAATTAGTAAGTAAGGAAATTAGGAAAGTGTG

FIGURE 42

>RevExon1\_TV1\_C\_ZAopt (SEQ ID NO:72)

ATGGCCGGCCGCAGCGGCACAGCGACGAGGCCCTGCTGCAGGTGGTGAAGATCATCAAGATCCTGTACCAGAGC

FIGURE 43

>RevExon1\_TV1\_C\_ZAwT (SEQ\_ID NO:73)

ATGGCAGGAAGAACGGAGACAGCGACGAAGCGCTCCTCCAAGTGGTAAAGATCATCAAAATCCTCTATCAAAGCA

FIGURE 44

>RevExon2\_TV1\_C\_ZAopt-2 (SEQ ID NO:74)

CCCTACCCCAAGCCCGAGGGCACCCGCCAGGCCGCCGCAACCGCCGCCGCTGGCGCGCCAGCGCCAGATCCA  
CACCATCGCGAGCGCATCCTGGTGGCTGCCTGGCCGAGCGCCGAGCCCCTGCAGCTGCCCCCTGGAGC  
GCCTGCACATCAACTGCAGCGAGGGCAGCGGCACCCAGCAGAGGCCAGGGCACCAACCGAGGGCGTGGCGAC  
CCCTAA

FIGURE 45

>RevExon2\_TV1\_C\_ZAwT (SEQ ID NO:75)

ACCCCTAACCCAAAGCCCGAGGGGACTCGACAGGCTGGAGGAATCGAAGAAGAAGGGTGGAGAGCAAGACAGAGACAGATC  
CATACGATTGGTGACCGGATTCTTGTGCGCTGGACGATCTGCGGAGCCTGTGCGCTTCACTACCAACCGCTTGA  
GAGACTTCATATTAAATTGCACTGAGGGCAGTGGAACTTCTGGACACAGCAGTCTCAGGGGACTACAGAGGGGTGGAG  
ATCCTTAA

FIGURE 46

the first and second class of the *Archaeopteryx* were the first to be described.

RT\_TV1\_C\_ZAopt (SEQ ID NO:76)

CCCATCAGCCCCATCGAGACCGTCCCCGTGAAGCTGAAGCCCCGATGGACGGCCCCA  
AGGTGAAGCAGTGGCCCCCTGACCGAGGAGAAGATCAAGGCCCTGACCGCCATCTGCG  
AGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGACAACCCCTACAACA  
CCCCCGTGTTCGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAGCTGGTGGACTT  
CCCGAGCTGAACAAAGCGCACCCAGGACTCTGGGAGGTGCAGCTGGCATCCCCCAC  
CCCGCCGGCTGAAGAAGAAGAGAGCTGACCGTGCTGGACGTGGCGACGCCTAC  
TTCAGCGTCCCCCTGGACGAGAGCTCCGCAAGTACACCGCCCTCACCATCCCCAGCA  
TCAACAACGAGACCCCCGGCATCCGCTACCAAGTACAACGTGCTGCCCAAGGGCTGGAA  
GGCAGCCCCGCCATCTTCAGAGCAGCATGACCAAGATCTGGAGGCCCTCCGCC  
AAGAACCCCGACATCGTATCTACCAAGTACATGGACGACCTGTACGTGGCAGCGACC  
TGGAGATCGGCCAGCACCAGCCAAGATCGAGGAGCTGCGCGAGCACCTGCTGAAGT  
GGGGCTTCACCACCCCCGACAAGAAGCACCAGAAGGAGCCCCCTCCTGTGGATGG  
CTACGAGCTGCACCCCGACAAGTGGACCGTGACGCCATCCTGCTGCCAGAGAACCG  
AGCTGGACCGTGAACGACATCCAGAAGCTGGTGGCAAGCTGAACACTGGCAGCCAG  
ATCTACCCCGCATCAAGGTGCGCCAGCTGTGCAAGCTGCTGCGCGGCCAAGGCC  
TGACCGACATCGTCCCCCTGACCGAGGAGGCCAGCTGGAGCTGGCGAGAACCGCG  
AGATCCTGCGCGAGCCCGTGCACGGCGTGTACTACGACCCAGCAAGGACCTGATCGC  
CGAGATCCAGAAGCAGGCCACGAGCAGTGGACCTACCAGATCTACCAAGGAGCCCT  
CAAGAACCTGAAGACCGGCAAGTACGCCAAGATGCGCACCAACCCACACCAACGACGT  
GAAGCAGCTGACCGAGGCCGTGCAGAAGATGCCATGGAGAGCATCGTATCTGGGG  
CAAGACCCCCAAGTTCCGCCATCCAGAAGGAGACCTGGAGACCTGGTGGACC  
GACTACTGGCAGGCCACCTGGATCCCCGAGTGGAGTTCGTAACACCCCCCCCCCTGG  
TGAAGCTGTGGTACCAGCTGGAGAAGGACCCATGCCGGCGTGGAGACCTTCTACGT  
GGACGGCGCCACCAACCGCGAGGCCAAGATCGGCAAGGCCGGTACGTGACCGACCG  
CGGCCGCCAGAAGATCGTACCGTACCCAGCAACACCAACCAACCAGAACGAGCTGCA  
GGCCATCCAGCTGCCCTGCAGGACAGCGCAGCGAGGTGAACATCGTACCGACAG  
CCAGTACGCCCTGGGCATCATCCAGGCCAGCCAGACAAGAGCGACAGCGAGATCTC  
AACCAGATCATCGAGCAGCTGATCAACAAGGAGCGCATCTACCTGAGCTGGGTGCCCG  
CCCACAAGGGCATCGCGGCCAACGAGCAGGTGGACAAGCTGGTGAGCAAGGGCATCC  
GCAAGGTGCTG

FIGURE 47

>RT\_TV1\_C\_ZAwT (SEQ ID NO:77)

CCAATTAGTCCTATTGAAACTGTACCACTAAACAGGAATGGATGCCAAAGGTCAAACAATGCCATTGAC  
AGAAGAAAAAATAAAGCATTAAACAGCAATTGTGAGGAATGGAGAAGGAAGGAAAATTACAAAATTGGCCTGATA  
ATCCATATAACACTCCAGTATTGCCATAAAAAGAAGGCAGTACTAAGTGGAGAAAATTAGTAGATTCAAGGAACCTC  
AATAAAAGAACTCAAGACTTTGGGAAGTTCAATTAGGAATACCACACCCAGCAGGATTAAAAAGAAAAATCAGTGAC  
AGTGCTAGATGTGGGGATGCATATTTTCAGTTCTTAGATGAAAGCTTCAGGAAATATACTGCATTACCATACCTA  
GTATAAACAAATGAAACACCAGGGATTAGATATCAATATAATGTGCTGCCACAGGGATGGAAAGGATCACCAAGCAATATTC  
CAGAGTAGCATGACAAAATCTTAGAGCCCTTCAGAGCAAAAATCCAGACATAGTTATCTATCAATATAATGGATGACTT  
GTATGTAGGATCTGACTTAGAAATAGGGCAACATAGAGCAAAATAGAAGAGTTAAGGGAACATTATTGAAATGGGAT  
TTACAACACCAGACAAGAACATCAAAAGAACCCCCATTCTTGGATGGGTATGAACTCCATCCTGACAATGGACA  
GTACAACCTATACTGCTGCCAGAAAAGGATAGTGGACTGTCATGATATAAGAAGTTAGTGGAAAATTAAACTGGC  
AAGTCAGATTACCCAGGGATTAAAGTAAGGCAACTCTGAAACTCCTCAGGGGCCAAAGCACTAACAGACATAGTAC  
CACTAAGTGAAGAACATTAGAATTGGCAGAGAACAGGGAAATTAAAGAGAACAGTACATGGAGTATATTATGAT  
CCATCAAAAGACTTGTAGCTGAAATACAGAAACAGGGCATGAACAATGGACATATCAAATTATCAAGAACCAATTAA  
AAATCTGAAAACAGGGAGTATGCAAAATGAGGACTACCCACACTAAATGATGTAACAGAGGCAGTGCAAA  
AAATAGCCATGAAAGCATAGTAATATGGGAAGACTCCTAAATTAGACTACCCATCCAAAAGAACATGGAGACA  
TGGTGGACAGACTATTGCAAGCCACCTGGATCCCTGAGTGGAGTTGTTAATACCCCTCCCTAGTAAATTATGTA  
CCAAGTAAAGATCCATAGCAGGAGTAGAAACTTCTATGTAGATGGAGCAACTAATAGGGAGCTAAATAGGAA  
AAGCAGGGTATGTTACTGACAGAGGAAGGCAGAAAATTGTTACTCTAACTAACACAACAAATAGAAGACTGAGTTACAA  
GCAATTCTAGCTCTGCAGGATTAGGATCAGAAGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCATTC  
AGCACAACCAGATAAGAGTGACTCAGAGATATTAAACCAATAATAGAACAGTTAATAACAAGGAAAGAACATCTACCTGT  
CATGGGTACCAGCACATAAAGGAATTGGGGAAATGAACAAGTAGATAATTAGTAAGTAAGGAATTAGGAAGTGTG

FIGURE 48

>RTmut\_TV1\_C\_ZAopt (SEQ ID NO:78)

CCCATCAGCCCCATCGAGACCGTGCCGTAAAGCTGAAGCCGGCATGGACGGCCCCAAGGTGAAGCAGTGGCCCCCTGAC  
CGAGGAGAAGATCAAGGCCCTGACGCCATCTGCGAGGAGATGGAGAAGGAGGGCAAGATCACCAAGATCGGCCCCGACA  
ACCCCTACAACACCCCCGTGTTGCCATCAAGAAGAAGGACAGCACCAAGTGGCGAAGCTGGTGGACTTCCCGAGCTG  
AACAAAGCGCACCCAGGACTTCTGGGAGGTGCAGCTGGGCATCCCCCACCCCGCCGGCTGAAGAAGAAGAAGAGCGTGAC  
CGTGTGGACGTGGCGACGCCCTACTTCAGCGTCCCCCTGGACGAGAGCTTCCGCAAGTACACCGCCTCACCATCCCCA  
GCATCAACAAACGAGACCCCCGGCATCGCTACCAAGTACAACGTGCTCCCCCAGGGCTGGAAGGGCAGCCCCGCCATCTC  
CAGAGCAGCATGACCAAGATCTGGAGCCCTCCGCGCCAAGAACCCGACATCGTATCTACCAGGCCCCCTGTACGT  
GGCAGCGACCTGGAGATCGGCCAGCACCGCCAAGATCGAGGAGCTGCGCGAGCACCTGCTGAAGTGGGCTTCACCA  
CCCCCGACAAGAACCGACCAAGGAGCCCCCTTCCTGCCATCGAGCTGCACCCGACAAGTGGACCGTGCAGCCCAC  
CTGCTGCCGAGAAGGACAGCTGGACCGTGAACGACATCCAGAACGCTGGTGGCAAGCTGAACCTGGCCACCCAGATCTA  
CCCCGGCATCAAGGTGCCAGCTGTGCAAGCTGCTGCCGGCGCCAAGGCCCTGACCGACATCGTCCCCCTGACCGAGG  
AGGGCGAGCTGGAGCTGGCGAGAACCGCGAGATCCTGCGCGAGCCCCCTGCACGGCGTGTACTACGACCCCAGCAAGGAC  
CTGATCGCGAGATCCAGAACGAGGGCCACGAGCAGTGGACCTACCAAGATCTACCAAGGAGCCCTCAAGAACCTGAAGAC  
CGGCAAGTACGCCAAGATGCGCACCACCCACACCAACGACGTGAAGCAGCTGACCGAGGCCGTGCAGAACGATGCCATGG  
AGAGCATCGTATCTGGGCAAGACCCCAAGTCCGCTGCCATCCAGAACGGAGACCTGGAGACCTGGTGGACCGAC  
TACTGGCAGGCCACCTGGATCCCCGAGTGGGAGTTCGTGAACACCCCCCTGGTGAAGCTGTGGTACCAAGCTGGAGAA  
GGACCCCATGCCGGCGTGGAGACCTTCTACGTGGACGGGCCACCAACCGCGAGGCCAAGATCGGCAAGGCCGGCTACG  
TGACCGACCGCGGCCAGAACGATCGTGAACCTGACCAACACCACCAAGAACGGAGCTGCAGGCCATCCAGCTG  
GCCCTGCAGGACAGCGGAGGTGAACATCGTACCGACAGCCAGTACGCCCTGGCATCATCCAGGCCAGCCGA  
CAAGAGCGACAGCGAGATCTCAACCAGATCATCGAGCAGCTGATCAACAAGGAGCGCATCTACCTGAGCTGGTGCCCG  
CCCACAAGGGCATCGCGCAACGAGCAGGTGGACAAGCTGGTGGACAGGGCATCCGCAAGGTGCTG

FIGURE 49

>RTmut\_TV1\_C\_ZAwT (SEQ ID NO:79)

CCAATTAGTCCTATTGAAACTGTACCACTGAAATGGATGGCCAAAGGTCAAACAATGCCATTGAC  
AGAAGAAAAAATAAAAGCATTAAACAGCAATTGTGAGGAATGGAGAAGGAAGGAAAATTACAAAATTGGGCCTGATA  
ATCCATATAACACTCCAGTATTGCCATAAAAAAGAAGGCAGTACTAAGTGGAGAAATTAGTAGATTCAGGGAACTC  
AATAAAAGAACTCAAGACTTTGGGAAGTCAATTAGGAATACCACACCCAGCAGGATTAAAAAGAAAAATCAGTGAC  
AGTGCTAGATGTGGGGATGCATATTTTCAGTCCTTAGATGAAAGCTTCAGGAAATATACTGCATTACCCATACTA  
GTATAAACATGAAACACCAGGGATTAGATATCAATATAATGTGCTGCCACAGGGATGAAAGGATCACCAGCAATATTC  
CAGAGTAGCATGACAAAAATCTTAGAGCCCTCAGAGCAAAATCCAGACATAGTTATCTATCAAGCCCCGTTGTATGT  
AGGATCTGACTTAGAAATAGGGCAACATAGAGCAAAATAGAAGAGTTAAGGGAACATTATTGAAATGGGATTACAA  
CACCAGACAAGAAACATCAAAAGAACCCCCATTCTCCATCGAACCTCCATCTGACAAATGGACAGTACAACCTATA  
CTGCTGCCAGAAAAGGATAGTGGACTGTCAATGATATACAGAAGTTAGTGGAAAATTAAACTGGCAAGTCAGATTAA  
CCCAGGGATTAAAGTAAGGCAACTCTGAAACTCTCAGGGGGCCAAAGCACTAACAGACATAGTACCAACTAAG  
AAGCAGAATTAGAATTGGCAGAGAACAGGGAAATTAAAGAGAACCCAGTACATGGAGTTATTGATCCATCAAAGAC  
TTGATAGCTGAAATACAGAAACAGGGCATGAACAATGGACATATCAAATTATCAAGAACCAATTAAAATCTGAAAC  
AGGGAAAGTATGCAAAATGAGGACTACCCACACTAATGATGTTAACAGAGGCAGTGCAAAAATAGCCATGG  
AAAGCATAGTAATATGGGAAAGACTCCTAAATTAGACTACCCATCCAAAAGAACATGGAGACATGGTGGACAGAC  
TATTGGCAAGCCACCTGGATCCCTGAGTGGAGTTGTTAATACCCCTCCCTAGTAAATTATGGTACCAACTAGAAA  
AGATCCCATAGCAGGAGTAGAAACTTTCTATGTAGATGGAGCAACTAATAGGGAGCTAAATAGGAAAGCAGGGTATG  
TTACTGACAGAGGAAGGCAGAAATTGTTACTCTAACTAACACAACAAATCAGAAGACTGAGTTACAAGCAATTCTAGCTA  
GCTCTGCAGGATTTCAGGATCAGAAGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATATTCAAGCACAACCAGA  
TAAGAGTGACTCAGAGATATTAAACCAATAATAGAACAGTTAATAAACACAAGGAAAGAATCTACCTGTATGGTACCA  
CACATAAAGGAATTGGGGAAATGAACAAGTAGATAAATTAGTAAGTAAGGAAATTAGGAAAGTGTGTTG

FIGURE 50

>TatC22Exon1\_TV1\_C\_ZAopt (SEQ ID NO:80)

ATGGAGCCGTGGACCCAAGCTGAAGCCCTGGAACCACCCGGCAGCCAGCCAAGACCGCCGGCAACAAC TGCTTCTG  
CAAGCACTGCAGCTACCACTGCCTGGTGTGCTTCCAGACCAAGGGCCTGGGCATCAGCTACGGCCGCAAGAAGCGCCGCC  
AGCGCCGCAGCGCCCCCCCCAGCGCGAGGACCACAGAACCCCCCTGAGCAAGCAG

FIGURE 51

>TatExon1\_TV1\_C\_ZAopt (SEQ ID NO:81)

ATGGAGCCCCTGGACCCCAAGCTGAAGCCCTGGAACCACCCGGCAGCCAGCCAAAGACCGCTGCAACAACTGCTTCTG  
CAAGCACTGCAGCTACCACTGCCTGGTGTGCTTCCAGACCAAGGGCCTGGGCATCAGCTACGGCCGCAAGAAGCGCCGCC  
AGCGCCGCAGCGCCCCCCCCAGCGGGGAGGACCAACCAAGAACCCCCCTGAGCAAGCAG

FIGURE 52

>TatExon1\_TV1\_C\_ZAwt (SEQ ID NO: 82)

ATGGAGCCAGTAGATCCTAAACTAAAGCCCTGGAACCCTCCAGGAAGCCAACTAAACAGCTTGTAAATAATTGCTTTG  
CAAACACTGTAGCTATCATTGCTAGTTGCTTTCAGACAAAAGGTTTAGGCATTTCTATGGCAGGAAGAAGCGGAGAC  
AGCGACGAAGCGCTCTCCAAGTGGTGAAGATCATCAAAATCCTCTATCAAAGCAG

FIGURE 53

>TatExon2\_TV1\_C\_ZAopt (SEQ ID NO:83)

CCCCTCCCCAGGCCGCGACAGCACCGCAGCGAGGAGAGCAAGAAGAAGGTGGAGAGCAAGACCGAGACCGACCC  
CTACGACTGGTGA

FIGURE 54

>TatExon2\_TV1\_C\_ZAw (SEQ ID NO:84)

CCCTTACCCCAAGCCCGAGGGGACTCGACAGGCTCGGAGGAATCGAAGAAGAAGGTGGAGAGCAAGACAGAGACAGATCC  
ATACGATTGGTGA

FIGURE 55

>Vif\_TV1\_C\_ZAopt (SEQ ID NO:85)

ATGGAGAACCGCTGGCAGGTGCTGATCGTGTGGCAGGTGGACCGCATGAAGATCCGCGCCTGGAACAGCCTGGTGAAGCA  
CCACATGTACATCAGCCGCCAGCGCTGGGTGACCGCCACCACCTCGAGAGCCGCCACCCCAAGGTGAGCAGCG  
AGGTGCACATCCCCCTGGCGACGCCCTGGTGTCAAGACCTACTGGGGCCTGCAGACCGCGAGCGCAGCTGGCAC  
CTGGGCCACGGCGTGAGCATCGAGTGGCGCCTGCAGCGAGTACAGCACCCAGGTGGACCCGACCTGGCGACCAGCTGAT  
CCACATGCACTACTTCGACTGCTTCACCGAGAGCGCCATCCGCCAGGCCATCCTGGGCCACATCGTGTCCCCGCTGCG  
ACTACCAGGCCACAAGAAGGTGGCAGCCTGCAGTACCTGGCCCTGACCGCCCTGATCAAGCCAAAGAAGCGCAAG  
CCCCCTGCCCAGCGTGCAGCTGGTGGAGGACCGCTGGAACGACCCCAAGAACCGCGGCCGGCAACCA  
CACCATGAACGCCACTAG

FIGURE 56

>Vif\_TV1\_C\_ZAwT (SEQ\_ID\_NO:86)

ATGGAAAACAGATGGCAGGTGCTGATTGTGTGGCAGGGACAGGATGAAGATTAGAGCATGGAATAGTTAGTAAAGCA  
CCATATGTATATATCAAGGAGAGCTAGTGGATGGGTCTACAGACATCATTTGAAAGCAGACATCCAAAAGTAAGTCAG  
AAGTACATATCCCATTAGGGATGCTAGATTAGTAATAAAACATATTGGGGTTGCAGACAGGAGAAAGAGATTGGCAT  
TTGGGTCTAGGAGTCTCCATAGAATGGAGACTGAGAGAATACAGCACACAAGTAGACCCCTGACCTGGCAGACAGCTAAT  
TCACATGCATTATTTGATTGTTTACAGAATCTGCCATAAGACAAGCCATATTAGGACACATAGTTTTCTAGGTGTG  
ACTATCAAGCAGGACATAAGAAGGTAGGATCTCTGCAATACTGGCACTGACAGCATTGATAAAACCAAAAAAGAGAAAG  
CCACCTCTGCCTAGTGTAGAAATTAGTAGAGGATAGGAAACGACCCCCAGAAGACCAGGGCCGCAGAGGGAACCA  
TACAATGAATGGACACTAG

FIGURE 57

>Vpr\_TV1\_C\_ZAopt (SEQ ID NO:87)

ATGGAGCGCCCCCGAGGACCAGGGCCCCAGCGCAGCCCTACAACGAGTGGACCTGGAGATCCTGGAGGAGCTGAA  
GCAGGAGGCCGTGCGCCACTTCCCCGCCCCTGGCTGCACAGCCTGGCCAGTACATCTACGAGACCTACGGCGACACCT  
GGACCGGCGTGGAGGCCATCATCCGCGTGCAGCAGCTGCTGTTCATCCACTTCCGATCGGCTGCCAGCACAGCCGC  
ATCGGCATCCTGCGCCAGCGCCGCCAACGGCGCCAGCCGCAGC

FIGURE 58

>Vpr\_TV1\_C\_ZAwt (SEQ\_ID NO:88)

ATGGAACGACCCCCAGAAGACCAGGGGCCGAGAGGAACCATACAATGAATGGACACTAGAGATTCTAGAAGAACTCAA  
GCAGGAAGCTGTCAGACACTTCCTAGACCATGGCTCCATAGCTTAGGACAATATATCTATGAAACCTATGGGATACCT  
GGACGGGAGTTGAAGCTATAATAAGAGTACTGCAACAACTACTGTTCAATTCAAGATTGGATGCCAACATAGCAGA  
ATAGGCATCTTGCACAGAGAAGCAAGAAATGGAGCCAGTAGATCC

FIGURE 59

>Vpu\_TV1\_C\_ZAopt (SEQ ID NO:89)

ATGGTGAGCCTGAGCCTGTTCAAGGGCGTGGACTACCGCCTGGCGCCCTGATCGTGGCCCTGATCATGCCAT  
CATCGTGTGGACCATCGCCTACATCGAGTACCGCAAGCTGGTGCAGCCAGAAGAAGATCGACTGGCTGATCAAGCGCATCC  
GCGAGCGCGCCGAGGACAGCGGCAACCGAGAGCGACGGCGACACCGAGGAGCTGAGCACCATGGTGGACATGGGCCACCTG  
CGCCTGCTGGACGCCAACGACCTGTAA

FIGURE 60

>Vpu\_TV1\_C\_ZAwT (SEQ ID NO:90)

ATGGTAAGTTAACGATTAAAGGAGTAGATTATAGATTAGGAGTAGGAGCATTGATAGTAGCACTAATCATAGCAAT  
AATAGTGTGGACCATAGCATATATAGAATATAGGAAATTGGAAGACAAAAGAAAATAGACTGGTTAATTAAAAGAATTA  
GGGAAAGAGCAGAAGACAGTGGCAATGAGAGTGATGGGGACACAGAAGAATTGTCAACAATGGTGGATATGGGCATCTT  
AGGCTTCTGGATGCTAATGATTGTAA

FIGURE 61

dna revexon1\_2TV1\_C\_ZAop (SEQ ID NO:91)

ATGGCCGGCCGCAGCGCGACAGCGACGAGGCCCTGCTGCAGGTGGTGAAGATCATC  
AAGATCCTGTACCAGAGCCCTACCCCAAGCCCGAGGGCACCCGCCAGGCCGCC  
ACCGCCGCCGCCGCTGGCGCGCCGCCAGCGCCAGATCCACACCATGGCGAGCGCAT  
CCTGGTGGCCTGCCTGGGCCGCAGCGCCGAGCCGTGCCCTGCAGCTGCCCTG  
GAGCGCCTGCACATCAACTGCAGCGAGGGCAGCGGCCACCAGCGGCACCCAGCAGAGC  
CAGGGCACCACCGAGGGCGTGGCGACCCCTAA

FIGURE 62

dna Revexon1\_2\_TV1\_C\_ZAw (SEQ ID NO:92)

ATGGCAGGAAGAAGCGGAGACAGCGACGAAGCGCTCCTCCAAGTGGTGAAGATCATC  
AAAATCCTCTATCAAAGCAACCCCTAACCCCAAGCCCCAGGGGACTCGACAGGCTCGGA  
GGAATCGAAGAAGAAGGTGGAGAGCAAGACAGAGACAGATCCATACGATTGGTGAGC  
GGATTCTTGTGCGCTGGGACGATCTGCGGAGCCTGTGCCTCTTCAGCTACCACCG  
CTTGAGAGACTTCATATTAAATTGCAGTGAGGGCAGTGGAACTTCTGGGACACAGCAGT  
CTCAGGGGACTACAGAGGGGTGGGAGATCCTTAA

FIGURE 63

dna TatC22Exon1\_2\_TV1\_C\_ZAopt (SEQ ID NO:93)

ATGGAGCCCCGTGGACCCCAAGCTGAAGCCCTGGAACCACCCGGCAGCCAGCCCAAG  
ACCGCCGGCAACAAC TGCTTCTGCAAGCACTGCAGCTACCACTGCCTGGTGTGCTTCC  
AGACCAAGGGCCTGGGCATCAGCTACGGCCGCAAGAAGCGCCGCCAGCGCCGCAGCG  
CCCCCCCCAGCGCGAGGACCACCAAGAACCCCTGAGCAAGCAGCCCCCTGCCAGGC  
CCGCGCGACAGCACCGGCAGCGAGGAGAGCAAGAAGAAGGTGGAGAGCAAGACCG  
AGACCGACCCCTACGACTGGTGA

FIGURE 64

dna TatExon1\_2\_TV1\_C\_ZAopt (SEQ ID NO:94)

ATGGAGCCCGTGGACCCAAGCTGAAGCCCTGGAACCACCCGGCAGCCAGCCCAAG  
ACCGCCTGCAACAACACTGCTTCTGCAAGCACTGCAGCTACCACTGCCTGGTGTGCTTCCA  
GACCAAGGGCCTGGCATCAGCTACGGCCGCAAGAACCCCTGAGCAAGCAGCCCCTGCCAGGCC  
CCCCCCAGCGCGAGGACCACCAGAACCCCTGAGCAAGCAGCCCCTGCCAGGCC  
GCGCGACAGCACCGGCAGCGAGGAGAGCAAGAACAGGTGGAGAGCAAGACCGAG  
ACCGACCCCTACGACTGGTGA

FIGURE 65

dna TatExon1\_2\_TV1\_C\_ZAwt (SEQ ID NO:95)

ATGGAGCCAGTAGATCCTAAACTAAAGCCCTGGAACCATCCAGGAAGCCAACCTAAA  
ACAGCTTGTAAATAATTGCTTTGCAAACACTGTAGCTATCATTGTCTAGTTGCTTCA  
GACAAAAGGTTAGGCATTCCTATGGCAGGAAGAAGCGGGAGACAGCGACGAAGCGC  
TCCTCCAAGTGGTGAAGATCATCAAAATCCTCTATCAAAGCAGCCCTACCCCCAAGCC  
CGAGGGGACTCGACAGGCTGGAGGAATCGAAGAAGAAGGTGGAGAGCAAGACAGA  
GACAGATCCATACGATTGGTGA

### FIGURE 66

卷之三

NefD125G-Myr\_TV1\_C\_ZAopt (SEQ ID NO:96)

ATGGCCGGCAAGTGGAGCAAGCGCAGCATCGTGGGCTGGCCCGCCGTGCGC  
GAGCGCATGCGCCGCCACCGAGGCCGCCGAGGGCTGGCGCCGCCAGC  
CAGGACCTGGACCGCCACGGCGCCCTGACCAGCAGCAACACCCCCGCCACCA  
ACGAGGCCTGCGCTGGCTGCAGGCCAGGAGGAGGACGGCGACGTGGGCT  
TCCCCGTGCGCCCCCAGGTGCCCTGCGCCCCATGACCTACAAGAGCGCCGT  
GGACCTGAGCTTCTTCCTGAAGGAGAAGGGCGGCCCTGGAGGGCCTGATCTAC  
AGCCGCAAGCGCCAGGAGATCCTGGACCTGTGGGTGTACAACACCCAGGGCT  
TCTTCCCCGGCTGGCAGAACTACACCAGCGGCCCGGCGTGCCTCCCCCTG  
ACCTTCGGCTGGTGCCTCAAGCTGGTCCCCTGGACCCCCCGCGAGGTGAAGG  
AGGCCAACGAGGGCGAGGACAACCTGCCTGCTGCACCCCCATGAGCCAGCACG  
GCGCCGAGGACGAGGACCGCGAGGTGCTGAAGTGGAAAGTTGACAGCCTGC  
TGGCCCACCGCCACATGGCCCGCGAGCTGCACCCCCGAGTACTACAAGGACTG  
CTGA

FIGURE 67

Envgp160\_TV2\_C\_ZAopt (SEQ ID NO:97)

ATGCGCGCCCGGGCATCCTGAAGAACTACGCCACTGGTGGATCTGGGCATCCT  
GGCTTCTGGATGCTGATGATGTGCAACGTGAAGGGCCTGTGGGTGACCGTGTACTA  
CGCGTGCCCGTGGGCCGAGGCCAAGACCACCCCTGTCGCGCAGCGACGCCA  
AGGCCTACGAGAAGGAGGTGCACAACGTGAGGCCACCCACGCCCTGCGTGCACC  
GACCCCAACCCCCAGGAGGTGATCCTGGCAACGTGACCGAGAACTTCAACATGTG  
GAAGAACGACATGGTGGACCAGATGCAGGAGGACATCATCAGCCTGTGGGACCGA  
GCCTGAAGCCCTGCGTGAAGCTGACCCCCCTGTCGCGTACCCCTGAACTGCACCAACG  
CCACCGTGAACATACAACACCAAGCAAGGACATGAAGAACTGCAGCTTACGTG  
ACCACCGAGCTGCGGACAAGAAGAAGAAGGAGAACGCCCTGTTCTACCGCCTGGA  
CATCGTCCCCCTGAACAAACCGCAAGAACGGCAACATCAACAAACTACCGCCTGATCA  
ACTGCAACACCAACAGCGCCATCACCCAGGCCTGCCCCAAGGTGAGCTCGACCCCATCC  
CCATCCACTACTGCGCCCCCGCCGCTACGCCCTGAAAGTGAACAAACAAGAAG  
TTCAACGGCATGGCCCCCTGCGACAACGTGAGCACCGTGCAGTGCACCCACGGCAT  
CAAGCCCCTGGTGGAGCACCCAGCTGCTGAAACGGCAGCCTGGCCGAGGAGGAGA  
TCATCATCCGAGCGAGAACCTGACCAACACGTGAAGAACCATCATCGTGCACCTG  
AACGAGAGCATCGAGATCAAGTGCACCCGGCAACAACACCCGCAAGAGCGT  
GCGCATGGCCCCGGCCAGGCCTTACGCCACCAGCTCAACTGCGGGCGAGTTCT  
GCCAGGCCACTGCAACATCAGCAAGAACGGAGTGGAACACACCACCCCTGAGCGCGT  
AGCCAGAAAGCTGCAGGAGCTGTTCCCAACAGCACGGCATCAAGTGCACCCCA  
CAGCGCGCGGCGACCTGGAGATCACCACCCACAGCTCAACTGCGGGCGAGTTCT  
TCTACTGCAACACCAACCGACCTGTTCAACAGCACCTACAGCAACGGCACCTGCACCA  
ACGGCACCTGCATGAGCAACAACACCGAGCGCATCACCCCTGAGTGCACATCAAG  
CAGATCATCAACATGTGGCAGGAGGTGGCCGCGCATGTACGCCCTCATCGC  
CGGCAACATCACCTGCCGAGCAACATCACCGCCGCTGCTGACCCGCGACGGCG  
GCGACAACAACACCGAGACCGAGACCTCCGCCGGCGGCGACATGCGCGAC  
AACTGGCGCAGCGAGCTGTACAAGTACAAGGTGGAGATCAAGCCCTGGCGT  
GGCCCCCACCAGGCCAAGCGCCGCGTGGTGGAGCGCGAGAACGGCGCCGTGGCA  
TCGGCGCCGTGTTCTGGCTTCTGGCGCCGCCGGCAGCACCATGGCGCCGCA  
GCATCACCTGACCGTGAGGCCAGCTGCTGAGCGCATCGTGCAGCAGCAG  
AGCAACCTGCTGCCGCCATCGAGGCCAGCAGCACATGCTGAGCTGACCGTGT  
GGGCATCAAGCAGCTGCAGGCCCGCGTGTGGCCATCGAGCGTACCTGCAGGACC  
AGCAGCTGCTGGGCTGTGGGCTGAGCGCAAGCTGATCTGCACCAACAGTG  
CTGTGGAACAGCAGCTGGAGCAACAAGACCCAGAGCGACATCTGGGACAACATGAC  
CTGGATGCACTGGGACCGCGAGATCAGCAACTACACCAACACCATACCGCCTGC  
TGGAGGACAGCCAGGCCAGCAGCAGGAGCGCAACGAGAACGGACCTGCTGGCCTGGA  
CCGCTGGAACAAACCTGTGGAACCTGGTCAAGCTGCTGAGCATCACCAACTGGCTGTGGTACATCAA  
GATCTTCATCATGATCGTGGCGGCCCTGATCGGCCCTGCGCATCATCTCGCCGTGCT  
GAGCCTGGTGAACCGCGTGCGCCAGGGCTACAGCCCTGAGCCTGAGACCCCTGA  
TCCCCAACCCCCGGGCCGACCGCCCTGGCGGCGATCGAGGAGGAGGGCGGCGAG  
CAGGACAGCAGCCGAGCATCCGCTGGTGGCGCTTCCGACCCCTGGCCTGGGA  
CGACCTGCGCAGCCTGTGCGCTGTTCTGCTACCCACCGCCTGCGCACTTCATCCTGAT  
CGTGGTGCAGCGCCGTGGAGCTGCTGGGCCACAGCAGCCTGCGCGCCCTGAGCGCG  
GCTGGGGCACCCCTGAAAGTACCTGGCAGCCTGGTGCAGTACTGGGGCTGGAGCTG  
AAGAAGAGCGCCATCAACCTGCTGGACACCACGCCATGCCATGCCGTGGCCGAGGGCAC  
CGACCGCATCCTGGAGTTCATCCAGAACCTGTGCCGCGCATCCGCAACGTGCCCG  
CCGCATCCGCCAGGGCTCGAGGCCGCGCCCTGAGTAA

FIGURE 68

ATGAGAGCGAGGGGGACTGAAGAATTATCGACACTGGTGGATATGGGCATCTT  
AGGCTTTGGATGCTAATGATGTGAATGTGAAGGGCTGTGGTCACAGTCTACTA  
CGGGGTACCTGTGGGGAGAGAAGCAAAAACACTCTATTTGTGCATCAGATGCTA  
AAGCATATGAGAAAGAAGTGCATAATGTCTGGCTACACATGCCTGTGTACCCACA  
GACCCCAACCCACAAGAAGTGAATTGGCAATGTAACAGAAAATTAAACATGTG  
GAAAAATGACATGGTGGATCAGATGCAGGAAGATATAATCAGTTATGGGATCAA  
GCCTTAAGCCATGTGTAAAATTGACCCCACCTCTGTGTCACTTAAACTGTACAAATG  
CAACTGTTAACTACAATAACCTCTAAAGACATGAAAAATTGCTTTCTATGTAA  
CCACAGAATTAAGAGATAAGAAAAAGAAAATGCACTTTTATAGAÇTTGAT  
ATAGTACCACTTAATAATAGGAAGAATGGGATATTAAACAACATAGATTAATAAA  
TTGTAATACCTCAGCCATAACACAAGCCTGTCCAAAAGTCTCGTTGACCCAATTCC  
TATACATTATTGTGCTCCAGCTGGTTATGCGCCTCTAAATGTAATAAAGAAAATT  
CAATGGAATAGGACCATGCGATAATGTCAGCACAGTACAATGTACACATGGAATT  
AGCCAGTGGTATCAACTCAATTACTGTTAAATGGTAGCCTAGCAGAAGAAGAGATA  
ATAATTAGATCTGAAAATCTGACAAACAATGTCAAAACAATAATAGTACATCTTAAT  
GAATCTATAGAGATTAAATGTACAAGACCTGGCAATAATACAAGAAAGAGTGTGAG  
AATAGGACCAGGACAAGCATTCTATGCAACAGGAGACATAATAGGAGATATAAGAC  
AAGCACATTGTAACATTAGTAAAAATGAATGGAATACAACCTTACAAAGGGTAAGT  
CAAAAATTACAAGAACTCTCCCTAATAGTACAGGGATAAAATTGCAACCACACTCA  
GGAGGGGACCTAGAAATTACTACACATAGCTTAATTGTGGAGGAGAATTTCAT  
TGCAATACAACAGACCTGTTAATAGTACATACAGTAATGGTACATGCACTAATGGT  
ACATGCATGTCTAATAATACAGAGCGCATCACACTCCAATGCAAGATAAAACAAAT  
TATAAACATGTGGCAGGAGGTAGGACGAGCAATGTATGCCCTCCATTGCAGGAA  
ACATAACATGTAGATCAAATTACAGGACTACTATTACACGTGATGGAGGAGAT  
AATAACTGAAACAGAGACATTGACACCTGGAGGAGACATGAGGGACAATTG  
GAGAAGTGAATTATAAATACAAGGTGGTAGAAATTAAACCATAGGAGTAGCAC  
CCACTGCTGCAAAAGGAGAGTGGTGGAGAGAGAAAAAGAGCAGTAGGAATAGG  
AGCTGTGTTCTGGGTTCTGGGAGCAGCAGGAAGCACTATGGCGCAGCATCAAT  
AACGCTGACGGTACAGGCCAGACAATTATTGTCTGGTATAGTGCACAGCAAAGTA  
ATTGCTGAGGGCTATAGAGGCAGCAACAGCATATGTCACACTACGGTCTGGGC  
ATTAAGCAGCTCCAGGCAAGAGTCCTGGCTATAGAGAGATACCTACAGGATCAACA  
GCTCCTAGGACTGTGGGCTGCTCTGGAAAACCTCATCTGCACCAACTAATGTGCTTTG  
GAACCTAGTTGGAGTAATAAAACTCAAAGTGTATTTGGATAACATGACCTGGAT  
GCAGTGGGATAGGGAAATTAGTAATTACACAAACACAATACAGGTTGCTGAAG  
ACTCGCAAAGCCAGCAGGAAAGAAATGAAAAAGATTACTAGCATTGGACAGGTGG  
AACAACTGTGGAATTGGTTAGCATAACAAATTGGCTGTGTATATAAAATATTC  
ATAATGATAGTAGGAGGCTTGATAGGTTAAGAATAATTGCTGTGCTCTCTCA  
GTAAATAGAGTTAGGCAGGGACTCACCCTGTCTGAGACCCCTATCCAAAC  
CCGAGGGGACCCGACAGGCTGGAGGAATCGAAGAAGAAGGTGGAGAGCAAGACA  
GCAGCAGATCCATTGATTAGTGGAGGATTCTGACACTGCCTGGACGACCTAC  
GAAGCCTGTGCCTCTGCTACCAACCGATTGAGAGACTTCATATTAAATTGTAGTGA  
GAGCAGTGGAACTTCTGGGACACAGTAGTCTCAGGGGACTGCAGAGGGGTGGGGA  
ACCCTTAAGTATTGGGGAGTCTTGCAATATTGGGGTCTAGAGTAAAAAGAGT  
GCTATTAACTGCTGATACTATAGCAATAGCAGTAGCTGAAGGAACAGATAGGATT  
CTAGAATTACACAAACCTTGTAGAGGTATCCGCAACGTACCTAGAAGAATAAG  
ACAGGGCTCGAAGCAGCTTGCAATAA

Gag\_TV2\_C\_ZAopt (SEQ ID NO:99)

ATGGGCGCCCGGCCAGCATCCTGCGCGGCCAGCAAGCTGGACAAGTGGAG  
AAGATCCGCCTGCGCCCCGGCGGCCAGCAAGCACTACATGCTGAAGCACCTGG  
TGTGGGCCAGCCGCGAGCTGGAGCGCTCGCCGTGAACCCGGCCTGCTGGA  
GACCAGCGACGGCTGCCGCCAGATCATCAAGCAGCTGCAGCCCCGCCCTGCAG  
ACCGGCACCGAGGAGATCCGAGCCTGTTCAACACCGTGGCCACCCCTGTACT  
GCGTGCACAAGGGCATCGACGTGCGCAGACACCAAGGAGGCCCTGGACAAGA  
TCGAGGAGGAGCAGAACAGTGCCAGCAGAAGACCCAGCAGGCCGAGGCCG  
CCGACAAGAAGGTGAGCCAGAACTACCCCATCGTCAGAACCTGCAGGGCC  
AGATGGTGCACCAGGCCATCAGCCCCCGCACCCCTGAACGCCCTGGGTGAAGGT  
GATCGAGGAGAAGGCCTCAGCCCCGAGGTGATCCCCATGTTCACCGCCCTG  
AGCGAGGGGCCACCCCCCAGGACCTGAACACCATGCTGAACACCGTGGGC  
GGCCACCAGGCCATGCAGATGCTGAAGGACACCATAACGAGGAGGCC  
GCCGAGTGGGACCGCTGCACCCGTGCACGCCGGCCCGTGGCCCCGCC  
AGATGCGCGAGCCCCGCCAGCGACATGCCGGCACCAACCAGCACCTGCA  
GGAGCAGATCGCCTGGATGACCAGCAACCCCCCATCCCCGTGGCGACATC  
TACAAGCGCTGGATCATCCTGGCCTGAACAAGATCGTGCATGTACAGCC  
CCGTGAGCATCCTGGACATCAAGCAGGGCCCAAGGAGCCCTTCCGCGACTA  
CGTGGACCGCTCTTCAAGACCCCTGCGCCGAGCAGAGCACCCAGGAGGTG  
AAGAACTGGATGACCGACACCCTGCTGGTGCAGAACGCCAACCCGACTGCA  
AGACCATCCTGCGCGCCCTGGCCCCCGGCCAGCCTGGAGGAGATGAC  
CGCCTGCCAGGGCGTGGCGGCCAGCCACAAGGCCCGTGTGGCCAG  
GCCATGAGCCAGGCCAACACACCAGCGTGTGATCCAGAACAGAGCAACTTC  
AAGGGCCCCGCCGCGCCGTGAAGTGCTCAACTGCGGCCGCGAGGGCCACA  
TCGCCCCGCAACTGCCGCCCGCAAGCGCGCTGCTGGAAGTGCAGGCAA  
GGAGGGCCACCAAGATGAAGGACTGCACCGAGCGCCAGGCCAACCTCCTGG  
CAAGATCTGGCCCAGCCACAAGGGCCGCCGGCAACTCCTGCAGAGGCC  
CCCGAGGCCACCGCCCCCCCCCTGGAGCCCACCGCCCCCGCCGAGAGCT  
TCAAGTTCAAGGAGACCCCAAGCAGGAGCCAAAGGACCGCGAGCCCCCTGA  
CCAGCCTGAAGAGCCTGTTGGCAGCGACCCCTGAGCCAGTAA

FIGURE 70

Gag\_TV2\_C\_ZAwt (SEQ ID NO:100)

ATGGGTGCGAGAGCGTCAATATTAAGAGGGGGAAAATTAGACAAATGGGAA  
AAAATTAGTTACGCCAGGGGGAGAAAACACTATATGCTAAAACACCTA  
GTATGGCAAGCAGAGAGCTGGAAAGATTGCAGTTAACCTGGCCTTTAG  
AGACATCAGACGGATGTAGACAAATAATAAAAACAGCTACAACCAGCTCTCA  
GACAGGAACAGAGGAATTAGATCATTATTAAACACAGTAGCAACTCTAT  
TGTGTACATAAAGGGATAGATGTACGAGACACCAAGGAAGCCTTAGACAAG  
ATAGAGGAGGAACAAAACAAATGTCAGCAAAAAACACAGCAGGCAGAAGCG  
GCTGACAAAAAGGTAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG  
AAATGGTACACCAGGCCATATCACCTAGAACCTTGAATGCATGGTAAAAGT  
AATAGAGGAGAAGGCTTCTAGCCCAGAGGTAATACCCATGTTACAGCATT  
TCAGAAGGAGCCACCCACAAGATTAAACACCATGTTAAATACAGTGGGG  
GACATCAAGCAGCCATGCAAATGTTAAAGATACCATCAATGAGGAGGCTGC  
AGAATGGTAGGTTACATCCAGTACATGCAGGGCTGTTGCACCAGGCCAG  
ATGAGAGAACCAAGGGGAAGTGACATAGCAGGAACACTACTAGTACCCCTCAA  
GAACAAATAGCATGGATGACAAGTAACCCACCTATCCAGTAGGGACATCT  
ATAAAAGGTGGATAATTCTGGGTTAAATAAAATAGTAAGAATGTACAGCCC  
TGTCAAGCATTCTAGACATAAAACAAGGACCAAGGAACCTTCTAGAGACTAT  
GTAGACCGGTTCTCAAAACTTAAGAGCTGAACAACTACAAGAGGTAA  
AAAATTGGATGACAGACACCTTGTAGTCCAAATGCGAACCCAGATTGAA  
GACCATTAAAGAGCATTAGGACCAGGGCTCATTAGAAGAAATGATGACA  
GCATGTCAGGGAGTGGAGGACCTAGCCACAAAGCAAGAGTTGGCTGAG  
GCAATGAGCCAAGCAAACAATACAAGTGTAAATGATACAGAAAAGCAATTAA  
AAGGCCCTAGAAGAGCTGTTAAATGTTCAACTGTGGCAGGGAGGGCACAT  
AGCCAGGAATTGCAGGGCCCTAGGAAAAGGGCTGTTGGAAATGTGGAAA  
GGAAGGACACCAAATGAAAGACTGTACTGAGAGGCAGGCTAATTCTAGGG  
AAAATTGGCCTTCCACAAGGGGAGGCCAGGGAAATTCTCAGAGCAGAC  
CAGAGCCAACAGCCCCACCACTAGAACCAACAGCCCCACCAAGCAGAGAGCT  
TCAAGTTCAAGGAGACTCCGAAGCAGGAGCCGAAAGACAGGGAACCTTAA  
CTTCCCTCAAATCACTCTTGGCAGCGACCCCTGTCTCAATAA

FIGURE 71

Nef\_TV2\_C\_ZAopt (SEQ ID NO:101)

ATGGGCGGCAAGTGGAGCAAGAGCAGCATCATCGGCTGGCCCGAGGTGCGC  
GAGCGCATCCGCCGCACCCGCAGCGCCGCCGAGGGCGTGGCAGCGCCAGC  
CAGGACCTGGAGAAGCACGGGCCCTGACCACCAGCAACACCGCCCACAAC  
AACGCCGCCTGCGCCTGGCTGGAGGCCAGGAGGAGGAGGGCGAGGTGGC  
TTCCCCGTGCGCCCCCAGGTGCCCTGCGCCCCATGACCTACAAGGCCGCAT  
CGACCTGAGCTTCTCCTGAAGGAGAAGGGCGGCCCTGGAGGGCCTGATCTAC  
AGCAAGAAGGCCAGGAGATCCTGGACCTGTGGGTGTACAACACCCAGGGC  
TTCTTCCCCGACTGGCAGAACTACACCCCCGGCCCCGGCGTGCCTCCCCCT  
GACCTTGGCTGGTACTTCAAGCTGGAGCCCGTGGACCCCCCGCAGGTGGAG  
GAGGCCAACGAGGGCGAGAACAACTGCCTGCTGCACCCCATGAGCCAGCAC  
GGCATGGAGGACGAGGACCGCGAGGTGCTGCGCTGGAAGTCGACAGCACC  
CTGGCCCCGCCACATGGCCCGCGAGCTGCACCCGAGTACTACAAGGACT  
GCTGA

FIGURE 72

Nef\_TV2\_C\_ZAwt (SEQ ID NO:102)

ATGGGGGGCAAGTGGTCAAAAAGCAGTATAATTGGATGGCCTGAAGTAAGA  
GAAAGAACATCAGACGAACTAGGTCAGCAGCAGAGGGAGTAGGATCAGCGTCT  
CAAGACTTAGAGAAACATGGGCACTTACAACCAGCAACACAGCCCACAAC  
AATGCTGCTTGCCTGGCTGGAAGCGCAAGAGGGAGGAAGGAGAAGTAGGC  
TTTCCAGTCAGACCTCAGGTACCTTAAGACCAATGACTTAAAGCAGCAAT  
AGATCTCAGCTCTTTAAAAGAAAAGGGGGACTGGAAGGGTTAATTAC  
TCCAAGAAAAGGCAAGAGATCCTGATTGTGGGTTATAACACACAAGGCT  
TCTCCCTGATTGGCAAAACTACACACCCGGACCAGGGTCAGATTCCACT  
GACCTTGGATGGTACTTCAAGCTAGAGCCAGTCGATCCAAGGGAAAGTAGAA  
GAGGCCAATGAAGGAGAAAACAACGTGTTACTACACCTATGAGCCAGCATG  
GAATGGAGGATGAAGACAGAGAAGTATTAGATGGAAGTTGACAGTACGC  
TAGCACCGCAGACACATGGCCCGAGCTACATCCGGAGTATTACAAAGACTG  
CTGA

FIGURE 73

Pol\_TV2\_C\_ZAopt (SEQ ID NO:103)

TTCTTCGCGAGAACCTGGCTTCCCCAGGGCGAGGCCCGAGTCCCCAGCGAGCAGACC  
CGCGCCAACAGCCCCACCACCGCACCAACAGCCCCACCAGCCCGAGCTGCAGGTGCAGGG  
CGACAGCGAGGCCGCCAGCGCCAGGGCACCTCAACTCCCCAGATCACCTGTGGC  
AGCGCCCCCTGGTGAGCATCAAGGTGGCCAGACCAAGGAGGCCAGTGGAAAGCCAAGATGATCGG  
GCCGACGACACCGTGTGGAGGAGATCAACCTGCCAGTGGAAAGCCAAGATGATCGG  
CGGCATCGCGGCTTCATCAAGGTGCCAGTACGACCAGATCCTGATCGAGATCTGCAGCA  
AGCGGCCATCGGCCACCGTGTGGGCCAGGGCACCCGTGAACATCATCGGCCAGACCTGC  
TGACCCAGCTGGCTGCACCCATGAACCTCCCCATCAGCCCCATCGAGACCGTGTGGCAG  
TGAAGCCGGCATGGACGGCCCCAAGGTGAAGCAGTGGCCCTGACCGAGGAGAAGATCAAG  
GCCCTGACCGAGATCTGCAGGGAGATGGAGAAGAGGGCAAGATACCAAGATCGGCCAG  
AGAACCCCTACAACACCCCCGTGTTGCCATCAAGAAGAAGGACAGCACCAAGTGGCGCAAG  
CTGGTGGACTTCCCGAGCTGAACAAGCGCACCCAGGACTCTGGAGGAGTGCAGCTGGCAG  
CCCCCACCCGCCCTGAAGAAGAAGAGACGGCTGACCGTGTGGACGTGGCAGGCC  
ACTTCAGCGTGCCCTGGACGAGAGCTCCGCAAGTACACCGCCTCACCATCCCCAGCATCA  
ACAACGAGACCCCCGGCATCCGCTACCAAGTACAACGTGCTGCCAGGGCTGGAAGGGAGC  
CCCGCCATCTCCAGAGCAGCATGACCCGATCCTGGAGCCCTCCGCAACCAAGAACCCGAG  
GTGGTGTACTACCAGTACATGGACGACCTGTACGTGGCAGCGACCTGGAGATCGGCCAGCA  
CCCGGCCAGATCGAGGAGCTGCCGGCACCTGCTGAAGTGGGCTTACCAACCCCCGACA  
AGAACGACCAAGAGGGAGCCCCCTTCCTGTGGATGGCTACGAGCTGACCCGACAAGTGG  
ACCGTGCAGCCATCCAGCTGCCAGAGAACGGAGAGCTGGACCGTGAACGACATCCAGAAGCT  
GGTGGCAAGCTGAACCTGGCCAGCCAGATCTACCCGGCATCAAGGTGCGCAGCTGTGCA  
AGCTGCTGCCGGCGCCAAGGCCCTGACCGACATCGTCCCCGACCGAGGAGGCCAGCTG  
GAGCTGGCCAGAACCGCGAGATCCTGAAGGAGGCCGTGACGGCGTGTACTACGACCCAG  
CAAGGACCTGATCGCCAGATCCAGAACGAGGGCACGACCAGTGGACCTACCAAGATCTACC  
AGGAGCCCTCAAGAACCTGCCGACCGCAAGTACGCCAGATGCCGACCGCCCACACCAAC  
GACGTGAAGCAGCTGCCAGGGCGTGCAGAACGATCACCCAGGAGAGCATCGTATCTGGGG  
CAAGACCCCCAAGTCCGCTGCCATCCCCAAGGAGACCTGGAGACCTGGTGGAGCGACT  
ACTGGCAGGCCACCTGGATCCCCGAGTGGAGTCTGTGAACACCCCCCTGGTGAAGCTGT  
GGTACCAAGCTGGAGAAGGAGCCATCGTGGGCCAGAACCTCTACGTGGACGGCGCC  
AACCGCGAGACCAAGATCGGAAGGCCCTACGTGACCGACAAGGGGCCAGAACGGTGG  
TGAGCTTCACCGAGACCAACCAGAACGAGCTGCAGGCCATCCAGCTGGCCCTGCAAG  
GACAGCGGCCCCGAGGTGAACATCGTACCGACAGCCAGTACGCCCTGGCAGATCCAGGC  
CCAGCCGACAAGAGCGAGAGCGAGCTGGTACGGCAGATCGAGCAGCTGATCAAGAAC  
GAGAACGGTGTACCTGAGCTGGTGCCCCACAAGGGCATGGCGCAACGAGCAGGTGGA  
CAAGCTGGTACCGAGCGGCATCCGCAAGGTGCTTCTGGACGGCATCGACAAGGCCAGG  
AGGAGCACGAGAACGATACCAACTGGCGGCCATGGCAGCGAGTCAACCTGCC  
ATCGTGGCCAAGGAGATCGTGGCCAGCTGCAGAACGCTGAAGGGCGAGGCCATGCA  
CGGCCAGGTGGACTGCAGCCCCGGCATCTGGCAGCTGGACTGCACCCACCTGGAGGGCAAGA  
TCATCCTGGTGGCCGTGCACGTGGCAGCGGCTACATGGAGGCCAGGTGATCCCCGCCAG  
ACCGGCCAGGAGACCGCCTACTTCATCTGAAGCTGGCCGGCGTGGCCCTGAGGTGATC  
CACACCGACAACGGCAGCAACTCACCAGCACGCCGTGAAGGCCCTGCTGGTGGCC  
CATCCAGCGAGTCCGGCATCCCCATCAACCCCCAGAGCCAGGGCGAGCACCTGAAAGACCGCC  
ACAAGGAGCTGAAGAACGATCATCGGCCAGGTGCGCAGCCAGGCGAGCACCTGAAAGACCGCC  
GTGCAGATGGCCGTGTTCATCCACAACCTCAAGCGCAAGGGCGCATCGCGGCTACAGCG  
CGCGAGCGCATCATCGACATCATCGCCAGCGACATCCAGACCAAGGAGCTGCAGAACGAGA  
TCATCAAGATCCAGAACACTCCCGCTGTACTACCGCGACAGCCGCAGGCCATCTGGAAAGGCC  
CCGCCAAGCTGCTGTGGAGGGCGAGGGCGCCGTGGTACCCAGGACAACAGCGACATCAAG  
GTGGTCCCCGCCAGGCCAGGAGGAGAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCC  
CTCGTGGCCGGCGCCAGGAGGAGAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCC

FIGURE 74

Pol\_TV2\_C\_ZAwT (SEQ ID NO:104)

TTTTTAGGGAAAATTGGCCTTCCCACAAGGGAGGCCAGGAATTCCCTCAGAGCAGACC  
AGAGCCAACAGCCCCACCACTAGAACCAACAGCCCCACCAGCAGAGAGCTCAAGTCAAGG  
AGACTCCGAAGCAGGAGCCGAAAGACAGGGAACCTTAACCTCCCTCAAATCACTCTTGGCA  
GCGACCCCTGTCTCAATAAAAGTAGCGGGCAAACAAAGGAGGCTCTTAGATACAGGAG  
CAGATGATACAGTACTAGAAGAAATAAACTGCCAGGAAATGAAACCAAAAATGATAGG  
AGGAATTGGAGGTTTATCAAAGTAAGACAGTATGATCAAATACTTATAGAAATTGTGGAAA  
AAGGGCTATAGGTACAGTATTAGTAGGACCTACACCTGTCAACATAATTGGAAGAAATCTGTT  
GACTCAGCTGGATGCACACTAAATTCCAATTAGCCCCATTGAAACTGTACCGAGTAAAATT  
AAAGCCAGGAATGGATGGCCAAAGGTTAACAAATGCCATTGACAGAAGAAAAATAAAA  
GCATTAACAGAAATTGTGAGGAAATGGAGAAGGAAGGAAAATTACAAAATTGGCCTGA  
AAATCCATATAACACTCCAGTATTGCCATAAAGAAGAAGGACAGTACAAAGTGGAGAAAAT  
TAGTAGATTTCAGGGAACTCAATAAAAGAACTCAAGACTTTGGGAAGTCCAATTAGGAATA  
CCACACCCAGCAGGGTTAAAAAAGAAAAAAATCAGTGACAGTACTGGATGTGGAGATGCATA  
TTTCAGTCCCTTAGATGAGAGCTTCAGAAAATACTGCATTACCCATACCTAGTATAAAC  
AATGAAACACCAAGGGATTAGATATCAATATAATTGTTCTCACAGGGATGAAAGGATCACC  
AGCAATATTCCAGAGTAGCATGACAAGAATCTTAGGCCATTAGAACACAAACCCAGAAG  
TAGTTATCTATCAATATATGGATGACTTATATGAGGATCTGACTTAGAAATAGGGCAACATA  
GAGCAAAATAAGAGGAGTTAAGAGGACACCTATTGAAATTGGGATTACACACCAGACAAG  
AAACATCAGAAAGAACCCCCATTCTTGGATGGGTATGAACTCCATCCTGACAAATGGACA  
GTACAGCCTATACAGCTGCCAGAAAGGAGAGCTGGACTGTCAATGATATACAGAAGTTAGT  
GGGAAAGTAAACTGGCAAGTCAGATTACCCAGGGATTAAAGTAAGGCAACTGTGAAAC  
TCCITAGGGAGCCAAAGCACTAACAGACATAGTCCACTGACTGAAGAAGCAGAATTAGAA  
TTGGCTGAGAACAGGGAAATTCTAAAAGAACAGTACATGGAGTATATTGACCCATCAAA  
AGATTTAATAGCTGAAATACAGAAACAGGGGAATGACCAATGGACATATCAAATTACCAAG  
AACCATTTAAAATCTGAGAACAGGAAGTATGCAAAAATGAGGACTGCCACACTAATGAT  
GTGAAACAGTTAGCAGAGGCACTGCAAAAGATAACCCAGGAAAGCAGATAGTAATATGGGAA  
AAACTCCTAAATTAGACTACCCATCCAAAAGAAACATGGGAGACATGGTGGTCAGACTATT  
GGCAAGCCACCTGGATTCCCTGAGTGGAGTTGTCATACCCCTCCCTAGTAAATTGTGGT  
ACCAGCTGGAAAAGAACCCATAGTAGGGGAGAAACTTCTATGTAGATGGAGCAGCCAAT  
AGGGAAACTAAAATAGGAAAGCAGGGTATGTCACTGACAAAGGAAGGCAGAAAGTTGTTTC  
CTCACTGAAACAACAAATCAGAACAGACTGAATTACAAGCAATTCTAGCTAGCTTGCAGGATT  
AGGCCAGAAGTAAACATAGTAACAGACTCACAGTATGCATTAGGAATCTAACAGCACAAAC  
CAGATAAGAGTGAATCAGAATTAGTCAGTCATAATAGAACAGTTGATAAAAAGGAAAAAA  
GTCTACCTATCATGGGTACCAGCACATAAAGGAATTGGAGGAAATGAAACAAGTAGACAAATT  
AGTAAGTAGTGGAAATCAGAAAAGTACTGTTCTAGATGGAATAGATAAAGCTCAAGAAGAGC  
ATGAAAATATCACAGCAATTGGAGAGCAATGGTAGTGGTTAATCTGCCACCCATAGTA  
GCAAAGGAAATAGTAGCCAGCTGTGATAATGTCAGCTAAAGGGGAAGCCATGCATGGACA  
AGTCGACTGTAGTCCAGGAATATGGCAATTAGACTGTACACATTAGAAGGAAAATCATCCT  
AGTAGCAGTCCATGTAGCCAGTGGCTACATGGAAAGCAGAGGTTATCCCAGCAGAAACAGGAC  
AAGAAACAGCATACTTATACAAATTAGCAGGAAGATGCCAGTCAGTAATACATACA  
GATAATGGCAGTAATTCAACAGTACCGCAGTTAAGGCAGCTGTTGGTGGCAGATATCCAA  
CGGGATTGGAATTCCCTACAATCCCCAAAGTCAGGAGTAGTAGAATCCATGAATAAAGA  
ATTAAGAAAATCATAGGGCAAGTAAGAGATCAAGCTGAGCACCTTAAGACAGCAGTACAAA  
TGGCAGTATTCAACATTAAAAGAAAAGGGGGATTGGGGGTACAGTCAGGGAG  
AGAATAATAGACATAATAGCATCAGACATACAAACTAAAGAATTACAAAACAAATTATAAA  
AATTCAAAATTTCGGTTTATTACAGAGACAGCAGAGACCCATTGGAAAGGACCAGCCAA  
ACTACTCTGGAAAGGTGAAGGGCAGTAGTAATACAGATAATAGTGTATAAAGGTAGTAC  
CAAGAAGGAAAGCAAAATCTAACAGACTATGGAAAACAGATGGCAGGTGCTGATTGTGTG  
GCAGGTAGACAGGATGAAGAT

FIGURE 75

RevExon1\_TV2\_C\_ZAopt (SEQ ID NO:105)

ATGGCCGGCCGCAGCGCGACAGCGACGAGGCCCTGCTGCAGGCCATCAAG  
ATCATCAAGATCCTGTACCAGAGC

FIGURE 76

RevExon1\_TV2\_C\_ZAwT (SEQ ID NO:106)

ATGGCAGGAAGAACGGAGACAGCGACGAAGCGCTCCTCCAAGCAATAAAG  
ATCATCAAGATCCTCTACCAAAGCA

FIGURE 77

RevExon2\_TV2\_C\_ZAopt (SEQ ID NO:107)

CCCTACCCCAAGCCCGAGGGCACCCGCCAGGCCGCCGCCAACCGCCGCC  
GCTGGCGCGCCGCCAGCAGCAGATCCACAGCATCAGCGAGCGCATCCTGGA  
CACCTGCCTGGGCCGCCACCAAGCCGTGCCCTGCTGCTGCCCCCCATCG  
AGGCCTGCACATCAACTGCAGCGAGAGCAGCGGCCACCAGCGGCACCCAGT  
AGAGCCAGGGCACCGCCGAGGGCGTGGGCAACCCCTAA

FIGURE 78

RevExon2\_TV2\_C\_ZAwt (SEQ ID NO:108)

ACCCTTATCCAAACCGAGGGACCCGACAGGCTCGGAGGAATCGAAGAA  
GAAGGTGGAGAGCAAGACAGCAGCAGATCCATTGATTAGTGAGCGGATTCT  
TGACACTTGCCTGGGACCTACGAAGCCTGTGCCTCTGCTACCACCGA  
TTGAGAGACTTCATATTAATTGTAGTGAGAGCAGTGGAACTCTGGGACACA  
GTAGTCTCAGGGGACTGCAGAGGGGTGGGAACCCTAA

FIGURE 79

TatExon1\_TV2\_C\_ZAopt (SEQ ID NO:109)

ATGGAGCCCATCGACCCAACCTGGAGCCCTGGAACCACCCGGCAGCCAGC  
CCAAGACCGCCTGCAACGGCTGCTACTGCAAGCGCTGCAGCTACCACTGCCT  
GGTGTGCTTCCAGAAGAAGGGCTGGGCATCTACTACGGCCGCAAGAACGCGC  
CGCCAGCGCCGCAGCGCCCCCCCCAGCAACAAGGACCACCAGGACCCCTGC  
CCAAGCAG

FIGURE 80

TatExon1\_TV2\_C\_ZAwt (SEQ ID NO:110)

ATGGAGCCAATAGATCTAACCTAGAACCCCTGGAACCATCCAGGAAGTCAGC  
CTAAAACGTGTTGTAATGGGTGTTACTGTAAACGTTGCAGCTATCATTGTCTA  
GTTTGCTTCAGAAAAAAGGCTAGGCATTACTATGGCAGGAAGAAGCGGA  
GACAGCGACGAAGCGCTCCTCCAAGCAATAAAGATCATCAAGATCCTCTACC  
AAAGCAG

FIGURE 81

TatExon2\_TV2\_C\_ZAopt (SEQ ID NO:111)

CCCCTGAGCCAGACCCGCGGCGACCCCACCGGCAGCGAGGAGAGCAAGAAG  
AAGGTGGAGAGCAAGACCGCCGCCGACCCCTTCGACTAG

FIGURE 82

TatExon2\_TV2\_C\_ZAwt (SEQ ID NO:112)

CCCTTATCCCAAACCCGAGGGGACCCGACAGGCTCGGAGGAATCGAAGAAG  
AAGGTGGAGAGCAAGACAGCAGATCCATTGATTAG

FIGURE 83

Vif\_TV2\_C\_ZAopt (SEQ ID NO:113)

ATGGAGAACCGCTGGCAGGTGCTGATCGTGTGGCAGGTGGACCGCATGAAGA  
TCCGCACCTGGCACAGCCTGGTGAAGCACCACATGTACGTGAGCCGCCGC  
CGACGGCTGGTTCTACCGCCACCACTACGAGAGGCCACCCCAAGGTGAGC  
AGCGAGGTGCACATCCCCCTGGCGACGCCGCCTGGTATCAAGACCTACT  
GGGGCCTGCAGACCGGCGAGCGCGCCTGGCACCTGGCACCGGCTGAGCA  
TCGAGTGGCGCCTGCGCCGCTACAGCACCCAGGTGGACCCGACCTGACCGA  
CCAGCTGATCCACATGCACTACTCGACTGCTCGCCGAGAGGCCATCGC  
AAGGCCATCCTGGCCAGATCGTGAGCCCCAAGTGCAGACTACCAGGCCGCC  
ACAACAAGGTGGGCAGCCTGCGACTACCTGGCCCTGACCGCCCTGATCAAGCC  
CAAGAAGATCAAGCCCCCTGCCAGCGTGCAGCTGGTGGAGGACCGC  
TGGAAACAAGCCCCAGAAGACCCGGCCGCCGGCAACCACACCATGAAC  
GGCCACTAG

FIGURE 84

Vif\_TV2\_C\_ZAwt (SEQ ID NO:114)

ATGGAAAACAGATGGCAGGTGCTGATTGTGTGGCAGGTAGACAGGATGAAG  
ATTAGAACATGGCACAGTTAGTAAAGCACCATATGTATGTTCGAGGAGAG  
CTGATGGATGGTCTACAGACATCATTATGAAAGCAGACACCCAAAAGTAAG  
TTCAGAAGTACACATCCCATTAGGAGATGCCAGGTTAGTAATAAAAACATAT  
TGGGGTCTGCAGACAGGAGAAAGAGCTGGCATTTGGGTACGGAGTCTCCA  
TAGAATGGAGATTGAGAAGATATAGCACACAAGTAGACCCCTGACCTGACAG  
ACCAACTAATTCATATGCATTATTTGATTGTTGCAGAATCTGCCATAAGG-  
AAAGCCATACTAGGACAGATAGTTAGCCCTAAGTGTGACTATCAAGCAGGAC  
ATAACAAGGTAGGATCTCTACAATAACTTGGCACTGACAGCATTGATAAAACC  
AAAAAAAGATAAAGCCACCTCTGCCTAGTGTAGGAAATTAGTAGAGGATAGA  
TGGAACAAGCCCCAGAAGACCAGGGGCCGAGAGGAACCATAATGAAT  
GGACACTAG

FIGURE 85

Vpr\_TV2\_C\_ZAopt (SEQ ID NO:115)

ATGGAGCAGGCCCGAGGACCAGGGCCCCAGCGCGAGCCCTACAACGAG  
TGGACCCCTGGAGCTGCTGGAGGAGCTGAAGCAGGAGGCCGTGCGCCACTTCC  
CCCGCCCCCTGGCTGCACAACCTGGGCCAGCACATCTACGAGACCTACGGCGA  
CACCTGGACCGGCGTGGAGGCCATCATCCGCATCCTGCAGCAGCTGCTGTT  
ATCCACTCCGCATCGGCTGCCACCACAGCCGCATGGCATTGCGCCAGC  
GCCGCGCCCGCAACGGCGCCAACCGCAGC

FIGURE 86

Vpr\_TV2\_C\_ZAwt (SEQ ID NO:116)

ATGGAACAAGCCCCAGAAGACCAGGGCCGCAGAGGAACCATAATGAA  
TGGACACTAGAGCTTTAGAAGAACTCAAGCAGGAAGCTGTCAGACACTTTC  
CTAGACCATGGCTCCATAACTTAGGACAACATATCTATGAAACCTATGGAGA  
TACTTGGACAGGAGTTGAAGCAATAATAAGAATCCTGCAACAATTACTGTTT  
ATTCATTTCAGGATTGGGTGCCATCAGCAGAATAGGCATTGCGACAGA  
GAAGAGCAAGAAATGGAGCCAATAGATCC

FIGURE 87

Vpu\_TV2\_C\_ZAopt (SEQ ID NO:117)

ATGCTGGACCTGACCGCCGCATCGACAGCCGCCTGGGCATCGGCGCCCTGA  
TCGTGGCCCTGATCATGCCCATCGTGTGGACATCGTGTACATCGAGTAC  
CGCAAGCTGGTGCGCCAGCGCAAGATCGACTGGCTGGTGAAGCGCATCCGCG  
AGCGCGCCGAGGACAGCGGCAACGAGAGCGAGGGCGACACCGAGGAGCTGA  
GCACCCCTGGTGGACATGGGCCACCTGCGCCTGCTGGACGCCAACGACGTGTA  
A

FIGURE 88

Vpu\_TV2\_C\_ZAwt (SEQ ID NO:118)

ATGTTAGATTAAC TGCAAGAATAGATTCTAGATTAGGAATAGGAGCATTGA  
TAGTAGCACTAATCATAGCAATAATAGTGTGGACCATAGTATATAGAATA  
TAGGAAATTGGTAAGGCAAAGGAAAATAGACTGGTTAGTTAAAAGGATTAG  
GGAAAGAGCAGAAGACAGTGGCAATGAGAGCGAGGGGGATACTGAAGAATT  
ATCGACACTGGTGGATATGGGGCATCTTAGGCTTGGATGCTAATGATGTGT  
AA

FIGURE 89

gp120mod.TV1.delV2 (SEQ ID NO:119)

1 gaattcatgc gcgtgatggg cacccagaag aactgccagc agtggtgat ctggggcatc  
61 ctgggcttct ggatgctgat gatctgcaac accgaggacc tgtgggtgac cgtgtactac  
121 ggcgtgcccc tgggcgca cgccaagacc accctgttct gcgccagcga cgccaaggcc  
181 tacgagaccg aggtgcacaa cgtgtggcc acccacgcct gcgtgcccac cgaccccaac  
241 ccccaggaga tcgtgtggg caacgtgacc gagaactca acatgtggaa gaacgacatg  
301 gcccaccaga tgcacgagga cgtgatcagc ctgtggacc agagcctgaa gcccgcgtg  
361 aagctgaccc ccctgtgcgt gaccctgaa tgcacccgaca ccaacgtgac cggcaaccgc  
421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcatctacaa catcgaggag  
481 atgaagaact gcagcttcaa cgccggcgcc ggccgcctga tcaactgcaa caccagcacc  
541 atcacccagg cctgccccaa ggtgagcttc gacccatcc ccatccacta ctgcgcccc  
601 gcccgcgtacg ccatctgaa gtcaacaac aagaccctca acggcaccgg cccctgtac  
661 aacgtgagca cctgtcagtg cacccacggc atcaagcccg tggtgagcac ccagctgctg  
721 ctgaacggca gcctggccga ggagggcatc atcatccgca gcgagaacct gaccgagaac  
781 accaagacca tcatctgca cctgaacgag agcgtggaga tcaactgcac ccccccac  
841 aacaacaccc gcaagagcgt ggcgcaccc cccggccagg cttctacgc caccacgcac  
901 gtgatcggca acatccgcca ggcccactgc aacatcagca cgcaccgtg gaacaagacc  
961 ctgcagcagg tcatgaagaa gctggcgag cactccccca acaagaccat ccagtcaag  
1021 ccccacggcg gggcgaccc ggagatcacc atgcacagct tcaactgcgc cggcgagttc  
1081 ttctactgca acaccagcaa cctgtcaac agcacctacc acagcaacaa cggcacctac  
1141 aagtacaacg gcaacagcag cagccccatc accctgcagt gcaagatcaa gcagatctg  
1201 cgcacgtggc agggcggtgg ccaggccacc tacgcccccc ccatcgccgg caacatcacc  
1261 tgccgcagca acatcaccgg catcctgtc acccgcgacg gggcttcaa caccaccaac  
1321 aacaccgaga cttccgccc cggcggcgac gacatgcgcg acaactggcg cagcgagctg  
1381 tacaagtaca aggtggtgaa gatcaagccc ctgggcattcg ccccccaccaa gccaagcgc  
1441 cgcgtggcgc agcgcgagaa ggcgtaactc gag

FIGURE 90

1 gaattcatgc gcgtgatggg caccagaag aactgccagc agtgggtggat ctggggcatc  
61 ctggcttctt ggatgctat gatctgcaac accgaggacc tgggggtgac cgtgtactac  
121 ggcgtgccccg tggcgccgca cgccaaagacc accctgttctt gcggcagcga cgccaaaggcc  
181 tacgagaccg aggtgcacaa cgtgtggcc acccacgcct gcgtgcccac cgaccccaac  
241 ccccaggaga tcgtgctggg caacgtgacc gagaacttca acatgtggaa gaacgacatg  
301 gccgaccaga tgcacgagga cgtgatcagc ctgtgggacc agagcctgaa gccctgcgtg  
361 aagctgaccc ccctgtgcgt gaccctgaac tgcaccgaca ccaacgtgac cggcaaccgc  
421 accgtgaccc gcaacacgac caacaacacc aacggcaccg gcatctacaa catcgaggag  
481 atgaagaact gcagttcaa cggccggccg gggccctgaa tcaactgcaa caccagcacc  
541 atcacccagg cctgccccaa ggtgagcttc gaccctatcc ccatccacta ctgcgcggcc  
601 gccggctacg ccatctgaa gtgcacaac aagacattca acggcaccgg cccctgtac  
661 aacgtgagca ccgtgcagt caccacggc atcaagcccg tggtagcac ccagctgctg  
721 ctgaacggca gcctggccgaa ggagggcatc atcatccgca gcgagaacct gaccgagaac  
781 accaagacca tcatctgca cctgaacgag agcgtggaga tcaactgac cccggccac  
841 aacaacaccc gcaagagcgt ggcacatggc cccggccagg ccttctacgc caccaacgac  
901 gtgatcggca acatccgcca ggcccactgc aacatcagca ccgaccgctg gaacaagacc  
961 ctgcagcagg ttagtgaagaa gctggggcag cacttccca acaagaccat ccagttaag  
1021 ccccacggc gggcgaccc ggagatcacc atgcacacgt tcaactgccc cggcgagttc  
1081 ttctactgca acaccagcaa cctgttcaac agcacctacc acagcaacaa cggcacccatc  
1141 aagtacaacg gcaacacgacg cagccccatc accctgcagt gcaagatcaa gcagatcgtg  
1201 cgcacgtggc agggcggtggg ccaggccacc tacggccccc ccatcgccgg caacatcacc  
1261 tgccgcagca acatcacggg catccgtctg acccgcgacg gggcttcaa caccaccaac  
1321 aacaccgaga ccttccggcc cggcgccggc gacatcgccg acaactggcg cagcgagctg  
1381 tacaagtaca aggtgggtgaa gatcaagccc ctgggcatcg ccccccaccaa ggccaagcgc  
1441 cgcgtggc acgcgcgagaa ggcgcgcgtg ggcacatcgccg ccgtgttccct gggcttctg  
1501 ggcggccggc gcagcaccat gggcgccgccc agcatcaccc tgaccgtgca ggcccggccag  
1561 ctgctgagcg gcatctgca gcaacgcacg aacctgcgtg aggccatcga ggcccacgag  
1621 cacatgcgtc agctgaccgt gtggggcatc aacgcacgtc aggccccgt gctggccatc  
1681 gagcgttacc tgaaggacca gcaacgtgt ggcacatctgg gctgcagcgg ccgcctgatc  
1741 tgcaccaccc cctgtccctg gaaacacgcg tggagcaaca agacgcgagaa ggacatctgg  
1801 gacaacatga cctggatgca gtggggaccgc gagatcagca actacacccgg cctgatctac  
1861 aacctgctgg aggacacggca gaaaccacgcg gagaagaacg agaaggaccc gctggagctg  
1921 gacaagtggaa acaaccctgtg gaactgggttc gacatcagca actggccctg gtacatctaa  
1981 ctcgag

FIGURE 91

gp140mod.TV1.mut7.delV2 (SEQ ID NO:121)

1 gaattcatgc gcgtgatggg cacccagaag aactgccagc agtggtgat ctggggcatc  
61 ctggcctctt ggtatgctgat gatctgcaac accgaggacc tgggggtgac cgtfactac  
121 ggcgtgcggc tggcgcgcga cgccaaagacc accctgttctt ggcgcagcga cgccaaaggcc  
181 tacgagaccg aggtgcacaa cgtgtggcc acccaacgcct ggcgtgcccac cgaccccaac  
241 ccccaggaga tcgtgtggg caacgtgacc gagaacttca acatgtggaa gaacgacatg  
301 gccgaccaga tgcacgagga cgtgtacgc ctgtgggacc agaggctgaa gcccgtcg  
361 aagctgaccc ccctgtgcgt gaccctgaac tgcaccgaca ccaacgtgac cggcaaccgc  
421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcatctacaa catcgaggag  
481 atgaagaact gcaaccttcaaa cgccggcgcc ggccgcctga tcaactgcaaa caccagcacc  
541 atcacccagg cctgccccaa ggtgagcttc gaccccatcc ccatccacta ctgcgcccc  
601 gcccgtacg ccatctgaa gtgcaacaac aagacccatca acggcaccgg cccctgtac  
661 aacgtgagca cctgtgcgtg caccacggc atcaagcccg tggtgagcac ccagctgt  
721 ctgaacggca gcctggccga ggagggcatc atcatccgca gcgagaacct gaccgagaac  
781 accaagacca tcatgtgca cctgaacggag agcgtggaga tcaactgcac ccgccccaaac  
841 aacaacaccc gcaagagcgt ggcgcacccgc cccggccagg ccttctacgc caccaacgcac  
901 gtgatcgca acatccgcca ggcccactgc aacatcagca cgcaccgtg gaacaagacc  
961 ctgcagcagg tggatggaa gctggcgag cacttttttca acaagaccat ccagtcaag  
1021 ccccacgccc gggcgaccc ggagatcacc atgcacagct tcaactgccc cggcgaggcc  
1081 ttctactgca acaccagcaa cctgttcaac agcacctacc acagcaacaa cggcacctac  
1141 aagtacaacg gcaacagcagc cagccccatc accctgcgt gcaagatcaa gcagatcgt  
1201 cgcacatgtggc agggcggtgg ccaggccacc tacggccccc ccatcgccgg caacatcacc  
1261 tgcccgagca acatcaccgg catcctgtg acccgcgacg gcccgttcaa caccaccaac  
1321 aacaccgaga cttccggcc cggcgccggc gacatgcgcg acaactggcg cagcgagctg  
1381 tacaagtaca aggtgggtgg gatcaaggccc ctgggcacatcg ccccccaccaa ggccatcagc  
1441 agcgtgggtgc agagcgagaa gagcgcgcgtg ggcacatggcg ccgtgttctt gggcttctg  
1501 ggcgcggccg gcagcaccat gggcgccggc agcatcaccc tgaccgtgca ggcccggcag  
1561 ctgcgtgacgc gcatctgca gcagcagagc aacctgtga aggccatcga ggcccagcag  
1621 cacatgctgc agctgaccgt gtggggcatc aagcagctgc aggcccgcgt gctggccatc  
1681 gagcgcgtacc tgaaggacca gcagctgtg ggcacatgtgg gctgcagcgg ccgcctgtac  
1741 tgcaccaccg ccgtgcctgtg gaacagcagc tggagcaaca agagcgagaa ggacatctgg  
1801 gacaacatga cctggatgca gtgggaccgc gagatcagca actacaccgg cctgtatctac  
1861 aacctgctgg aggacagccaa gaaccagcag gagaagaacg agaaggaccc gctggagctg  
1921 gacaagtggaa acaacctgtg gaactgggttc gacatcagca actggccctg gtacatctaa  
1981 ctgcag

FIGURE 92

gp160mod.TV1.delV1V2 (SEQ ID NO:122)

1 gaattcatgc gcgtgatggg cacccagaag aactgccagc agtggtgat ctggggcatc  
61 ctgggttctt ggatgctat gatctgcaac accgaggacc tgtgggtgac cgttactac  
121 ggcgtgcccgg tggcgccgca cgccaaagacc accctgttctt ggcgcggcga cgccaaaggcc  
181 tacgagaccg aggtgcacaa cgtgtggcc accccacgcct ggcgtgcccac cgaccccaac  
241 ccccaaggaga tcgtgttggg caacgtgacc gagaacttca acatgtggaa gaacgacatg  
301 gccgaccaga tgcacgagga cgttgcacgc ctgtgggacc agagcctgaa gcccgtcg  
361 aagctgaccc ccctgtgcgt gggcgccggc aactgcaaca ccaggcaccat cacccaggcc  
421 tgcccaagg tgagttcga cccatcccc atccactact ggcgcggc cggctacgccc  
481 atcctgaagt gcaacaacaa gaccccaac ggcacccggcc cctgctacaa cgttgcaccc  
541 gtgcagtgc cccacggcat caagcccggt gtgagcaccc agtgcgtgtt gacccggc  
601 ctggccgagg agggcatcat catccgcggc gagaacctga ccgagaacac caagaccatc  
661 atcgtgcacc tgaacgagag cgtggagatc aactgcaccc gccccaaacaa caacaccgc  
721 aagagcgtgc gcatccggcc cggccaggcc ttctacgcca ccaacgacgt gatccggcaac  
781 atccgcagg cccactgcaaa catcggcacc gaccgcttgg acaagaccctt gcaaggatgg  
841 atgaagaagc tggcgagca ttcccaac aagaccatcc agtcaagcc ccacccggc  
901 ggcgacccgg agatcaccat gcacagcttc aactggcgcc gcgagttctt ctactgcaac  
961 accagcaacc ttgttcaacag caccttaccatc agcaacaacg gcacccatcaa gtacaacggc  
1021 aacagcagca gccccatcac cctgcagtgc aagatcaacg agatcgatgcg catgtggcag  
1081 ggcgtggcc agggccacca cggccggccatc acatccatcg cccggcggc  
1141 atcaccggca ttctgttgc acggcggccggc ggcgttcaaca ccaccaacaa caccggacc  
1201 ttccggccggc gggcgccgca catcgccgac aactggcgca gcgagctgtt caagtacaag  
1261 gtggggaga tcaagccctt gggcatcgcc cccaccaagg ccaagccggc cgtgggtgc  
1321 cgcgagaagc ggcggcgtggg catcgccgac gtgttgcgtt gcttgcgtt cggccggcc  
1381 agcaccatgg ggcggccggc catcaccctt accgtgcagg cccggccatc gctgagcc  
1441 atcgtgcagc agcagagcaaa cctgttgcag gccatcgagg cccggccatc catgtgc  
1501 ctgaccgtgtt gggccatcaa gcaatcgccggc gcccggccgtt tgccatcgatc ggcgttcc  
1561 aaggaccagc agtgcgtggg catctggggc tgcaatcgcc ggcgtatcg caccaccgc  
1621 gtgccttggg acagcagctt gggccatcaa gcaatcgcc ggcgtatcg caccaccgc  
1681 tggatgcgtt gggccatcaa gcaatcgccggc tacaccggcc tgatctacaa cctgttgc  
1741 gacagccaga accagcagga gaagaacgag aaggaccgtt tggatgcgtt caatgttgc  
1801 aacccgttggg actgggttgcg catcgccatc tggcccttggt acatcaagat ctccatcat  
1861 atcgtggccggc gcctgttgcg cctgcgcacatc atcttcggcc tgctgagcat cgttgc  
1921 gtgcggccagg gtcacagccccc cctgttgcgtt cagacccttga ccccccggcc cccggcc  
1981 gaccggccgtt gggccatcgatc ggaggaggcc gggcgccagg accggccatc cggccatcc  
2041 ctggatgcgtt gcttgcgtt gggccatcgatc gcaatcgcc ggcgtatcg cctgttgc  
2101 taccaccggcc tgcgttgcgtt cagacccttga ccccccggcc cccggcc  
2161 agcaggccatc ggcggccgtt gggccatcgatc ggaggaggcc gggcgccatc cggccatcc  
2221 cagtttttttggg ggcgttgcgtt gggccatcgatc gcaatcgcc ggcgtatcg cccggcc  
2281 accgtggccggc agggccatcgatc gggccatcgatc gggccatcgatc ggcgtatcg  
2341 ctgaacatcc cccggccatcgatc gggccatcgatc gggccatcgatc ggcgtatcgatc

FIGURE 93

gp160mod.TV1.delV2 (SEQ ID NO:123)

1 gaattcatgc gcgtgatggg cacccagaag aactgccagc agtggtgat ctggggcatc  
61 ctggcttct ggtgctgat gatctgcaac accgaggacc tgggtgtac cgtgtactac  
121 ggcgtgcccgtgtggcgca cgccaagacc accctgtct gcgccagcga cgccaaggcc  
181 tacgagaccg aggtgcacaa cgtgtggcc acccacgcct gcgtgcccac cgaccccaac  
241 cccaggaga tcgtgctggg caacgtgacc gagaacttca acaftggaa gaacgacatg  
301 gcccaccaga tgcacgagga cgtgatcagc ctgtggacc agagctgaa gcccgcgt  
361 aagctgaccc ccctgtcggt gaccctgaac tgcaccgaca ccaacgtgac cggcaaccgc  
421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcatctacaa catgaggag  
481 atgaagaact gcagctcaa cgccggcgc ggcgcctga tcaactgcaa caccagcacc  
541 atcacccagg cctgccccaa ggtgagcttc gaccccatcc ccatccacta ctgcgcccc  
601 gcccggctacg ccatctgaa gtgcaacaac aagaccttca acggcaccgg cccctgctac  
661 aacgtgagca cctgtcgatg cacccacggc atcaagecccg tggtgagcac ccagctgt  
721 ctgaacggca gcctggccga ggaggccatc atcatccgca gcgagaacct gaccgagaac  
781 accaagagcca tcatctgca cctgaacggag agcgtggaga tcaactgac cccggccaaac  
841 aacaacaccc gcaagagcgt ggcacatggc cccggccagg cttctacgc caccaacgac  
901 gtgatcggca acatccgcca gcccactgc aacatcagca cggaccgctg gaacaagacc  
961 ctgcagcagg tcatgaagaa gctggcgag cacttccca acaagaccat ccagttcaag  
1021 cccacgccc gggcgaccc ggagatcacc atgcacagct tcaactgccc cggcgagttc  
1081 ttctactgca acaccagcaa cctgttcaac agcacctacc acagcaacaa cggcacctac  
1141 aagttacaacg gcaacagcag cagccccatc accctgcgt gcaagatcaa gcagatctg  
1201 cgcacatgtggc agggcgatggg ccaggccacc tacggccccc ccatcgccgg caacatcacc  
1261 tgccgcagca acatcaccgg catcctgtc acccgccgacg gcccgttcaa caccaccaac  
1321 aacaccgaga cttccgccc cggccggcgc gacatcgccg acaactggcg cagcgagctg  
1381 tacaagtaca aggtggtggaa gatcaagccc ctggcatcg ccccccaccaa ggccaagcgc  
1441 cgcgtggtgc agcgcgagaa ggcgcgcgtg ggcacatggc cctgttcctt gggcttcctg  
1501 ggcgcgcgc gcaagcaccat gggccgcgc accatcaccc tgaccgtgca gggccgcag  
1561 ctgcgtgagcg gcatctgca gcacgcgacg aacctgtga aggccatcg ggcgcgcag  
1621 cacatctgca agctgaccgt gtggggcatc aagcagctgc aggccccgt gctggccatc  
1681 gagcgctacc tgaaggacca gcaagctgtc ggcacatctgg gctgcagcgg cccctgtatc  
1741 tgcaccaccg ccgtggctgtg gaacgcgcgc tggagcaaca agagcgagaa ggacatctgg  
1801 gacaacatgaa cttggatgca gtggggccgc gagatcagca actacaccgg cctgtatctac  
1861 aaccctgtgg aggacagcca gaaccagcag gagaagaacg agaaggaccc tggagactg  
1921 gacaagtggaa acaacctgtg gaactggttc gacatcagca actggccctg gtacatcaag  
1981 atcttcatca tggatgtgggg cggccgtatc ggcctgcgc tcatcttcgc cttgtgagc  
2041 atcgtaacc ggcgtgcgc gggctacagc cccctgagct tccagaccct gaccccccagc  
2101 ccccgccgc tggaccgcctt gggccgcacg gaggaggagg gggccgcgc gggccgcac  
2161 cgcacatcc gcgtggtag cggccgttgc accctggccctt gggacgcaccc ggcacaccc  
2221 tgccgttca gtcaccaccg cctgcgcgc ttcatctgtc tgccgtgcgc cggccgtggag  
2281 ctgcgtggcc acagcagcctt ggcgcgcctg cagcgccgc gggagatccctt gaagtaccctg  
2341 ggcgcgcgtt gtcagactgt gggccgtggag ctgaagaaga ggcgcgcgc cctgtggac  
2401 accatcgcca taccatgtggc cgaggccacc gaccgcacca tgcagctgtt gcaacgcac  
2461 tgccgcgc tccatgtggccat ccccgccgc atccgcagg gttcgaggc cggccgtgt  
2521 taactcgag

FIGURE 94

gp160mod.TV1.mut7.delV2 (SEQ ID NO:124)

1 gaattcatgc gcgtgatggg caccagaag aactgccagc agtggtgat ctggggcatc  
61 ctggctctt ggtatgtat gatctgcaac accgaggacc tgggtgtac cggttactac  
121 ggcgtccccg tggcgccgca cgccaaagacc accctgttctt ggcgcagcga cgccaaaggcc  
181 tacgagaccg aggtgcacaa cgtgtggcc acccacgcctt ggcgtccccac cgaccccaac  
241 cccaggaga tcgtgctggg caacgtgacc gagaacttca acatgtggaa gaacgacatg  
301 gcccggcaga tgcacgagga cgtgatcagc ctgtgggacc agagcctgaa gcccgtcg  
361 aagctgaccc ccctgtcggtt gaccctgaac tgcaccgaca ccaacgtgac cggcaaccgc  
421 accgtgaccc gcaacagcac caacaacacc aacggcaccg gcatctacaa catcgaggag  
481 atgaagaact gcagctcaa cgcggcgcc ggccgcctga tcaactgcaaa caccagcacc  
541 atcacccagg cctgccccaa ggtgagcttc gaccctatcc ccatccacta ctgcgcccc  
601 gcccgtacg ccatcctgaa gtgcaacaac aagaccttca acggcaccgg cccctgtac  
661 aacgtgagca cctgtcgatg caccacggc atcaagcccg tggtgagcac ccagctgt  
721 ctgaacggca gcctggccgaa ggaggccatc atcatccgca gcgagaacctt gaccgagaac  
781 accaagagcca tcacgtgca cctgaacccg agcgtggaga tcaactgcaac cggccccaaac  
841 aacaacaccc gcaagagcgt ggcacatggc cccggccagg cttctacgc caccacgac  
901 gtgatcggca acatccgcca ggcccactgc aacatcagca cggaccgctg gaacaagacc  
961 ctgcagcagg tggatggaa gctggcgag cactttccca acaagaccat ccagtcaag  
1021 cccacggccg gggcgaccc ggagatcacc atgcacagct tcaactgccc cggcgagg  
1081 ttctactgca acaccagcaa cctgttcaac agcacctacc acagcaacaa cggcacctac  
1141 aagtacaacg gcaacagcag cagccccatc accctgcgtt gcaagatcaa gcagatcg  
1201 cgcacatgtggc agggcggtgg ccagggcacc tacggcccccc ccatcgccgg caacatcacc  
1261 tgccgcagca acatcaccgg catcctgtt acccgcgacg gcccgttcaa caccaccaac  
1321 aacaccgaga ccttccggcc cggcggcgcc gacatcgccg acaactggcg cagcgagct  
1381 tacaagtaca aggtgggtgg gatcaagccc ctggcatcg ccccccaccaa ggccatcag  
1441 agcgtggcgtc agagcgagaa gagcggcggtt ggcacatggc cccgtttctt gggcttct  
1501 ggcggccggc gcaagcaccat gggcgccggcc agcataccct tgaccgtca gggccggc  
1561 ctgcgtgacg gcatcgca gcaacggcagc aacctgttca accgttccatc ggcacccgg  
1621 cacatgtgc agctgaccgtt gtggggcatc aagcagctgc agggccggcgt gctggccatc  
1681 gagcgttacc tgaaggacca gcaacgtgtt ggcacatgtt gctgcagcgg cccctgtatc  
1741 tgcaccaccg ccgtggccctg gacacggcagc tggagcaaca agacggagaa ggacatctgg  
1801 gacaacatga cctggatgca gtggggccgc gagatcagca actacaccgg cctgtatctac  
1861 aacctgttgg aggacagcca gaaccaggcag gagaagaacg agaaggaccc tggagact  
1921 gacaagtggaa acaacctgtt gacactggatc gacatcagca actggccctg gtacatcaag  
1981 atcttcatca tggatgtggg cggccgttgc ggcctgcgc tcatcttcgc cttgtgt  
2041 atcgtgaacc ggcgtggccca gggctacagc cccctgttgc tccagaccctt gacccccc  
2101 ccccgccggcc tggaccggcc gggcgccatc gaggaggagg gggcgagca ggacccgg  
2161 cgcacatcc gcgtggcgatc gggcttctg agcctggccctt gggacgaccc ggcaccc  
2221 tgcctgttca gtcaccaccg cctgcgcgc ttcacatcttca tcgcgttgc ggcgtgg  
2281 ctgcgtggcc acagcagcc ggcgtggccctg cagcgccggcgtt gggagatccatc  
2341 ggcacccctgg tgcgtgttgc gggccgtggag ctggatggaa ggcaccc  
2401 accatcgcca tcaaccgtggc gggccggccacc gaccgttca tggatgttgc gca  
2461 tgcacgtggccca tccatgttgc tggatggaa gggccggccacc  
2521 taactcgag

FIGURE 95

gp160mod.TV1.tpa1 (SEQ ID NO:125)

1 gtcgacgcca ccatggatgc aatgaagaga gggctctgct gtgtgctgct gctgtgtgga  
61 gcagtcttcg ttcccccag cgccagcacc gaggaccgt gggtgaccgt gtactacggc  
121 gtccccgtgt ggccgcacgc caagaccacc ctgttctgct ccagcgacgc caaggccatc  
181 gagaccgagg tgcacaacgt gtggccacc cacgcctgct tgcccaccga ccccaacccc  
241 caggagatcg tgctggcaa cgtgaccgag aactcaaca tgtgaaagaa cgacatggcc  
301 gaccagatgc acgaggacgt gatcagccctg tgggaccaga gcctgaagcc ctgcgtgaag  
361 ctgacccccc tgcgtgtac cctgaactgc accgacacca acgtgaccgg caaccgcacc  
421 gtgaccggca acagcaccaa caacaccaac ggcacccggca tctacaacat cgaggagatg  
481 aagaactgca gcttcaacgc caccaccgag ctgcgcgaca agaagcacaa ggagtacgcc  
541 ctgttctacc gcctggacat cgtccccctg aacgagaaca gcgacaactt cacctaccgc  
601 ctgatcaact gcaacaccag caccatacc caggcctgcc ccaagggtgag ctgcgtacccc  
661 atccccatcc actactgcgc ccccgccggc tacgccatcc tgaagtgcaa caacaagacc  
721 ttcaacggca cggccccctg ctacaacgtg agcaccgtgc agtgcacccca cgccatcaag  
781 cccgtggta gcacccagct gctgctgaac ggcagccctgg ccgaggaggg catcatcattc  
841 cgcagcgaga acctgaccga gaacaccaag accatcatcg tgcacccctgaa cgagagcgtg  
901 gagatcaact gcacccgccc caacaacaac acccgcaaga gcgtgcgtat cgccccggc  
961 caggccttct acgcccaccaa cgacgtgatc ggcaacatcc gccaggccca ctgcaacatc  
1021 agcaccgacc gctggaacaa gaccctgcag caggtgatga agaagctggg cgagcacttc  
1081 cccaaacaaga ccatccagtt caagccccac gccggcggcg acctggagat caccatgcac  
1141 agcttcaact gccgcggcga gttttctac tgcaacacca gcaacctgtt caacagcacc  
1201 taccacagca acaacggcac ctacaagtac aacggcaaca gcagcagccc cataccctg  
1261 cagtgcaga a tcaagcagat cgtgcgcattt tgccaggcg tggccaggc caccatgcgc  
1321 ccccccattcg cggcaacat caccgcgc agcaacatca cggcattctt gtcacccgc  
1381 gacggcggct tcaacaccac caacaacacc gagaccccttcc gccccggcg cggcgacatg  
1441 cgcgacaact ggcgcagcga gctgtacaag tacaagggtgg tggagatcaa gcccctggc  
1501 atgcccccc ccaaggccaa ggcgcgcgtg gtgcagcgcg agaagcgcgc cgtgggcattc  
1561 ggcgcgtgt tcctggcattt cctggcgcc gccggcagca ccatggcgcc cgccagcatc  
1621 accctgaccg tgcaggcccg ccagctgcgt agcggcatcg tgcagcagca gagcaacctg  
1681 ctgaaggccaa tggggccca gcaaggccatcg tgcagctga ccgtgtggg catcaaggcag  
1741 ctgcaggccc gcgtgcgtgc catcgagcgc tacctgaagg accaggcagct gtcgggcattc  
1801 tggggctgca ggcgcgcctt gatctgcacc accgcgcgtc cctggaaacag cagctggagc  
1861 aacaagagcg agaaggacat ctgggacaac atgaccctgaa tgcagttggg cccgcgagatc  
1921 agcaactaca cggccctgat ctacaacccctg ctggaggaca gccagaacca gcaggagaag  
1981 aacgagaagg acctgctgaa gctggacaag tggaaacaacc tgcgttggactt gttcgacatc  
2041 agcaactggc cctggatcat caagatcttc atcatgatcg tggccggcctt gatccgcgt  
2101 cgcacatct tgcgtgtgt gacatcgatc aaccgcgtgc gccaggccatc cagcccccctg  
2161 agcttcaga ccctgacccca cagccccccgc ggcctggacc gcctggcgccatcgaggag  
2221 gagggcggcg agcaggaccg cgaccgcgcg atccgcgtgg tgagcggcattt cctgagccctg  
2281 gcctggacacg acctgcgcacaa cctgtgcctt ttcagctacc accgcctgcgc cgacttcatc  
2341 ctgatgcgc tgcgcgcgtt ggagctgcgtt ggcgcacagca gcctgcgcgg cctgcgcgc  
2401 ggctggaga tcctgaagta cctggccagc ctgggtgcagt actggggcctt ggagctgaag  
2461 aagagcgcca tcagccgtctt ggacaccatc gccatcaccgc tggccggagg caccgaccgc  
2521 atcatcgagc tgggtgcagcg catctgcgcg gccatcctga acatccccccgc cgccatccgc  
2581 caggccttcg agggcccccctt gtcgttactc gag

FIGURE 96

gp160mod.TV1 (SEQ ID NO:126)

1 gaattcatgc gcgtgatggg caccaggaa aactgcccgc agtgggtggat ctggggcata  
61 ctgggcttct ggtatgctgat gatctgcaac accggaggacc tgtgggtgac cgtgtactac  
121 ggcgtccccg tgtggcgca cgccttgcgc accctgttct gcgcctgcgc cgccttgcgc  
181 tacgagaccg aggtgcacaa cgtgtggcc acccacgcct gcgtgcccac cgaccccaac  
241 cccctggaga tcgtgttgc caacgtgacc gagaacttca acatgtggaa gaacgacatg  
301 gcccggaga tgcacgagga cgtgttgcgc ctgtgggacc agagcctgaa gcccgttgc  
361 aagctgaccc ccctgtgcgt gaccctgaa tgcaccgaca ccaacgtgac cggcaaccgc  
421 accgtgaccc gcaacagcac caacaacacc aacggcaccg gcatctacaa catcgaggag  
481 atgaagaact gcagcttcaa cgccaccacc gagctgcgc acaagaagca caaggagtag  
541 gcccgttct accgccttgc catctgcgc ctgaacgaga acagcgacaa ctccacccat  
601 cgcctgatca actgcaacac cagcaccatc acccaggcct gccttgcgtt gagcttgcac  
661 cccatccccca tccactactg cggccggcc gcgtacgcca tcctgaagtg caacaaca  
721 accttcaacg gcacccggcc ctgttacaac gtgagccacc tgcatgtgcac ccacggcata  
781 aagccctgtgg tgagccacca gctgtgttgc aacggcagcc tggccgagga gggcatatc  
841 atccgcagcg agaaccttgc acgagaacacc aagaccatca tcgtgcaccc gaacgagagc  
901 gtggagatca actgcacccgc ccccaacaac aacacccgc aagacgtgcgc catggcccc  
961 ggccttgcgttccatgcac caacgttgc atcggcaaca tcggccaggc ccactgcaac  
1021 atcagcaccg accgcttgcgaa caagaccctg cagcaggatg tgaagaagct gggcgagcac  
1081 tccttcaaca agaccatcca gttcaagccc cacggccggcg ggcacccatggaa gatcaccatcg  
1141 cacagcttca actgcccggcg cgagtttccatgc acaccatccatggaa gatcaccatcg  
1201 acctaccaca gcaacaacgg cacccatcaag tacaacggca acagcagcag cccatcacc  
1261 ctgcgttgcgca agatcaaga gatctgcgc atgtggcagg gctgtggccca ggcacccat  
1321 gccccccccca tcggccggaa catcaccatgc cgcacccatggaa gatcaccatcg  
1381 cggacccggcg gcttcaacac caccaacaac accgagacccatggaa gatcaccatcg  
1441 atgcgcgaca actggcgccag cgagctgttgc aagttacaagg tgggtggat caagccctg  
1501 ggcacccatggaa gatcaccatcgcc ccaccaaggc caagccggccgc gttgtgcgc ggcacccatgg  
1561 atcggccggcg tgggtggccatggaa gatcaccatcgcc ccaccaaggc  
1621 atcaccatcgcc gatcaccatcgcc ccaccaaggc gatcaccatcgcc  
1681 ctgcgttgcgca agtgcgttgc acaccatcgcc gatcaccatcgcc  
1741 cagctgcagg cccgcgttgc gatcaccatcgcc gatcaccatcgcc  
1801 atcggggcttgc gatcaccatcgcc ccaccaaggc gatcaccatcgcc  
1861 agcaacaaga gatcaccatcgcc gatcaccatcgcc  
1921 atcagcaact acaccatcgcc gatcaccatcgcc  
1981 aagaacgaga gatcaccatcgcc gatcaccatcgcc  
2041 atcagcaact acaccatcgcc gatcaccatcgcc  
2101 ctgcgttgcacccatcgcc gatcaccatcgcc  
2161 ctgcgttgcacccatcgcc gatcaccatcgcc  
2221 gatcaccatcgcc gatcaccatcgcc  
2281 ctgcgttgcacccatcgcc gatcaccatcgcc  
2341 atcctgttgc gatcaccatcgcc gatcaccatcgcc  
2401 cggccgtggg gatcaccatcgcc gatcaccatcgcc  
2461 aagaagagcg ccatcaccatcgcc gatcaccatcgcc  
2521 cggccgtggg gatcaccatcgcc gatcaccatcgcc  
2581 cggccgtggg gatcaccatcgcc gatcaccatcgcc

FIGURE 97

gp160mod.TV1.wtLnative (SEQ ID NO:127)

1 gaattcatga gagtgatggg gacacagaag aattgtcaac aatggtgat atggggcatc  
61 ttaggettctt ggatgctaat gatttgtaac accgaggacc tggggtgac cgtgtactac  
121 ggcgtccccg tggcgccgca cgccaaagacc accctgttct ggcgcagcga cgccaaaggcc  
181 tacgagaccc aggtgcacaa cgtgtggcc acccacgcct gctgtcccac cgaccccaac  
241 cccaggaga tcgtgctgg caacgtgacc gagaacttca acatgtggaa gaacgacatg  
301 gccgaccaga tgcacgagga cgtgatcgc ctgtgggacc agagcctgaa gcccgcgt  
361 aagctgaccc ccctgtgcgt gaccctgaac tgcaccgaca ccaacgtgac cggcaaccgc  
421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcatctacaa catcgaggag  
481 atgaagaact gcagctcaa cgccaccacc gagctgcgcg acaagaagca caaggagttac  
541 gcccgttct accgcctgga catcgccctt ctaacgaga acagcgacaa cttcacctac  
601 cgcctgatca actgcaacac cagcaccatc acccaggccct gccccaaagggt gagcttcgac  
661 cccatccccca tccactactg cggcccccggc ggctacgcca tcctgaagtg caacaacaag  
721 acctcaacg gcaccggccc ctgctacaac gtgagcaccg tgcagtgcac ccacggcatc  
781 aagccctgtgg tgagcaccctt gctgctgtt aacggcagcc tggccgagga gggcatcatc  
841 atccgcagcg agaacctgac cgagaacacc aagaccatca tcgtgcacccctt gaacgagagc  
901 gtggagatca actgcacccg ccccaacaac aacacccgcg agagcgtgcg catggcccc  
961 ggcaggccct tctacgcccac caacgacgtt atcggcaaca tccgcccaggcc ccaactgcaac  
1021 atcagcacccg accgctggaa caagaccctg cagcagggttga tgaagaagctt gggcgagcac  
1081 ttcccccaaca agaccatcca gttcaagccc cacggccggc ggcacccctt gatcaccatc  
1141 cacagcttca actgcccggc cgagttctt tactgcaaca ccagcaacccctt gttcaacagc  
1201 acctaccaca gcaacaacgg cacctacaag tacaacggca acagcagcag ccccatcacc  
1261 ctgcagtgcac agatcaagca gatcgccgc atgtggcagg gcgtggccca ggcacccctt  
1321 gccccccccca tcgcccggcaaa catcaccctgc cgcagcaaca tcaccggcat cctgctgacc  
1381 cgcgcggcg gcttcaacac caccaacaac accgagacccctt cccggccggc cggccggcgac  
1441 atgcgcgaca actggcgccag cgagctgttca aagtacaagg tggggatcaagccctt  
1501 ggcaccccccaccccaagggc caagcggccgc gtggcggcgc ggcgagaagcg cggccgtggc  
1561 atcggcgcccg tggccctggg ctccctggc gcccggca gacccatggg cggccggccac  
1621 atcacccttca cctgcggccggc cccggccggc ctgagcggca tcgtgcggca gcaaggccac  
1681 ctgctgaagg ccatcgaggcc ccaaggccac atgctgcggc tgaccgtgtt gggcatcaag  
1741 cagctgcagg cccgcgtgtt ggcacccgtt cgcgttccatgca aggaccagca gctgtggc  
1801 atctggggctt gcaaggcccg cctgatctgc accaccggccg tggccctggaa cagcagctgg  
1861 agcaacaaga ggcgagaagggc catctgggac aacatgacccctt ggttgcgtt ggcgaccc  
1921 atcagcaactt acaccggccctt gatctacaac ctgctggagg acagccagaa ccaggccagg  
1981 aagaacgaga aggacccgtt ggcacccgtt ggcacccgtt ggcacccgtt cgggttcgac  
2041 atcagcaactt ggcacccgttca catcaagatc ttcatcatca tcgtggccgg cctgatcgcc  
2101 ctgcgcacatca ttttcggccgtt gctgaggcatc gtggccggc tggccctgggg ctacagcccc  
2161 ctgagcttcc accaccctgcac ccccgccccc cggccgttcc accaccggccctt ggcgacttcc  
2221 gaggaggccg ggcgacccgtt cccggccggc accatccgcctt tggccggccgg cttccctgg  
2281 ctggccctggg accaccctgcac caacccgttca ctgctggccgtt accaccggccctt ggcgacttcc  
2341 atccctgatcg ccgtgcggccg cgtggacccgtt ctggccggccca gcaaccgttcc cggccgttcc  
2401 cggccgtggg agatcttca gttacccgttcc accaccggccgtt ggttgcgtt ggcaccc  
2461 aagaagagccg ccatcgaccctt gctggacacc atcggccatca cctggccggca gggccaccc  
2521 cgcacatcatcg agctgggttca ggcacatctgc cgcacccatcc tggccctgggg ctggccgttcc  
2581 cggccaggccgtt tcgaggccggc cctgctgttca ctggccgtt

FIGURE 98

Wild-type Env gp160 (8\_2\_ZA) (SEQ ID NO:128)

1 atgagagtga tggggacaca gaagaattgt caacaatggc ggatatggg catcttagc  
61 ttctgatgc taatgattt taacacggag gactgtggg tcacagtcta ctatgggta  
121 cctgtgtgaa gagacgcaaa aactactcta ttctgtcat cagatctaa agcatatgag  
181 acagaagtgc ataatgtctg ggctacacat gcctgtgtac ccacagaccc caacccacaa  
241 gaaaatgttt tggaaatgt aacagaaaat ttaaatatgt ggaaaaatgt aatggcagat  
301 cagatgcattt aggtatgtt cttttatgg gatcaaagcc taaagccatg tgtaaagtt  
361 accccactct gtgtcacttt aaactgtaca gatacaatgt ttacaggtaa tagaactgtt  
421 acaggtataa gtaccaataa tacaaatgtt acaggtattt ataacattgt aagaaatgaaa  
481 aattgcttcaatgcac cacagaatta agagataaga aacataaaga gtatgcactc  
541 tttatagac ttgatatagtt accacttaat gagaatagt acaactttac atatagatta  
601 ataaattgca ataccaatcataacaccaaa gcctgtccaa aggtcttttg tgacccgatt  
661 cctatacatt actgtgctcc agctggtttgcgattctaa agtgtataa taagacattc  
721 aatgggacag gaccatgtta taatgtcagc acagtacaat gtacacatgg aattaagcca  
781 gtggatcaa ctaattact gttaaatgtt agtcttagcag aagaagggat aataatttaga  
841 tctgaaaatt tgacagagaa tacccaaaca ataatagtac accttatgt aatctgttagag  
901 attaattgtca caagacccaa caataataca agaaaaatgt taaggatagg accaggacaa  
961 gcattctatg caacaatgt tgtaatagga aacataagac aagcacattg taacatttagt  
1021 acagatagat ggaacaaaac ttacaacag gtaataaaaa aataggaga gcattccct  
1081 aataaaacaa tacaatttaa accacatgcggatgggatgggat aatgcata  
1141 ttaattgtca gaggagaatt ttctattgtt aatacatcaaa acctgtttaa tagcacatac  
1201 cactctaata atggatcata caaatacaat ggttaatcaa gtcacccat cacactccaa  
1261 tgtaaaataa aacaaattgtt acgtatgtgg caaggggttag gacaagcaac gtatgccct  
1321 cccattgcag gaaacataac atgttagatca aacatcacag gaatactatt gacacgtgt  
1381 ggaggattta acaccacaaa caacacagag acattcagac ctggaggagg agatatgagg  
1441 gataactgttca gaagtgttcaatataatataaaat aaagttagttag aaattaagcc attgggata  
1501 gcacccacta aggcaaaaag aagagtggcagagagaaa aaagagcagt ggaaatagga  
1561 gctgtgttcc ttgggttctt gggagcagca ggaagcacta tggcgccagc gtcaataac  
1621 ctgacggatc aggccagaca actgttgc tttatgtgc aacagcaaaag caatttgctg  
1681 aaggctatag aggcgcacaca gcatatgtt caactcacag tctggggcat taagcagctc  
1741 caggcgagag tctggctat agaaagatac ctaaaggatc aacagcttcc agggattttgg  
1801 ggctgtctg gaagactcat ctgcaccact gctgtgcctt ggaactccag ttggagtaat  
1861 aaatctgaaa aagatatttg ggataacatg acttggatgc agtggatag agaaatttagt  
1921 aattacacag gcttaatata caattgttca gaaactcggc aaaaccagca ggaaaaagaat  
1981 gaaaaagatt tatttagaatt ggacaatgtt aacaatctgtt ggaattgggtt tgacatatca  
2041 aactggccgt ggtatataaa aatattcata atgatagtag gaggcttgc aggtttaaaga  
2101 ataaatttttgcgtgtttc tataatgttca gaggatggc agggataactc acctttgtca  
2161 ttccagaccc ttaccccaag cccgaggggta ctcgcacaggc tcggaggaat cgaagaagaa  
2221 ggtggagagc aagacagaga cagatccata cgattggta ggcggatctt gtgcgttgc  
2281 tgggacgatc tgccgttacactt gtcgttgc tgcgttgc tgcgttgc  
2341 attgcgttca gggcgttgcgatc acttctggta cacagcgttc tcaaggactt acagagggg  
2401 tggaaatcc ttaagtatctt gggaaatgtt gtcgttgc tgcgttgc tgcgttgc  
2461 agtgcgttca gtcgttgc taccatagca ataacatgtt gtcgttgc tgcgttgc  
2521 atagaatttag tacaaagaat ttgttagatgtt atcctcaaca tacatgttca aataagac  
2581 ggctttgttca gggcgttgc tgcgttgc tgcgttgc tgcgttgc

FIGURE 99

gp140mod.TV1.tpa1 (SEQ ID NO:131)

1 atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt  
61 tcgcccagcg ccagcaccga ggacctgtgg gtgaccgtgt actacggcgt gcccgtgtgg  
121 cgcgacgcca agaccaccct gttctgcgcc agcgacgcca aggctacga gaccgagggtg  
181 cacaacgtgt gggccaccca cgcctgcgtg cccaccgacc ccaacccca ggagatcgtg  
241 ctggcaacg tgaccgagaa ctcaacatg tggaagaacg acatggccga ccagatgcac  
301 gaggacgtga tcagcctgtg ggaccagagc ctgaagccct gctgtgaagct gaccccccgt  
361 tgcgtgaccc tgaactgcac cgacaccaac gtgaccggca accgcaccgt gaccggcaac  
421 agcaccaaca acaccaacgg caccggcatc tacaacatcg aggagatgaa gaactgcac  
481 ttcaacgcca ccaccgagct gcgcgacaag aagcacaagg agtacgcct gttctaccgc  
541 ctggacatcg tgcccctgaa cgagaacagc gacaacttca cctacccgt gatcaactgc  
601 aacaccagca ccatcaccca ggcctcccc aaggtgagct tcgacccat ccccatccac  
661 tactgcgcc cgcgcggcta cgcctccgt aagtgcacaca acaagacctt caacggcacc  
721 ggcccctgct acaacgtgag caccgtgcag tgcacccacg gcatcaagcc cgtggtgagc  
781 acccagctgc tgctgaacgg cagcctggcc gaggagggca tcatcatcg cagcgagaac  
841 ctgaccgaga acaccaagac catcatcgta caccgtgaaagc agagcgfcca gatcaactgc  
901 acccgccccca acaacaacac cgcacagac gtgcgcacgt gccccggcca ggccttctac  
961 gccaaccaacg acgtgatcg caacatccgc cagggccact gcaacatcg caccgaccgc  
1021 tggaacaaga ccctgcagca ggtgatgaaag aagctggcg agcacttccc caacaagacc  
1081 atccagttca agcccccacgc cggcggcgac ctggagatca ccatgcacag ctcaactgc  
1141 cgcggcgagt tcttctactg caacaccagc aacctgtca acagcaccta ccacagcaac  
1201 aacggcacct acaagtacaa cggcaacagc agcagccccca tcaccctgca gtgcagatc  
1261 aagcagatcg tgcgcacgtg gcagggcggt ggcacggcca cctacggccc ccccatcgcc  
1321 gccaacatca cctgcccgcag caacatcacc ggcacccgtc tgacccgcgca cggcggcttc  
1381 aacaccacca acaacaccga gacccctccgc cccggcgccg ggcacatcg cgacaactgg  
1441 cgcacgcgac tgcgtacaagta caagggtgggtg gagatcaagc ccctggccat cgcccccacc  
1501 aaggccaagc gccgcgtggt gcagcgccgag aagcgcgcgc tgccatcg cgccgtgttc  
1561 ctggcttcc tggcgccgc cggcagcacc atggcgccg ccagcatcac cctgaccgt  
1621 caggccccgc agctgctgag cggcatcgta cagcagcaga gcaacctgt gaaaggccatc  
1681 gaggccccagc agcacaatgt gcagctgacc gtgtgggca tcaagcagct gcaggcccgc  
1741 gtgcgtggcca tcgagcgcata cctgaaggac cagcagctgc tggccatctg gggctgcagc  
1801 gcccgcctga tctgcaccac cggccgtcccc tggaaacagca gctggagcaa caagagcgag  
1861 aaggacatct gggacaacat gacctggatc cagtgccgacc gcgagatcg caactacacc  
1921 ggcctgatct acaacctgt ggaggacagc cagaaccagc aggagaagaa cgagaaggac  
1981 ctgcgtggagc tggacaagtg gaacaacctg tggaactggt tcgacatcg caactggccc  
2041 tggtatcatct aa

FIGURE 100

gp140mod.TV1 (SEQ ID NO:132)

1 gaattcatgc gcgtgatggg cacccagaag aactgccagc agtggtgat ctggggcatc  
61 ctggcttct ggtatgtat gatctgcaac accgaggacc tgtgggtgac cgtgtactac  
121 ggcgtcccg tgtggcgca cgccaagacc accctgttct gcgccagcga cgccaaggcc  
181 tacgagaccg aggtgcacaa cgtgtggcc acccacgcct gcgtgcccac cgaccccaac  
241 ccccaggaga tcgtgctggg caacgtgacc gagaacttca acatgtggaa gaacgacatg  
301 gccgaccaga tgcacgagga cgtgatcagc ctgtgggacc agagcctgaa gccctgcgt  
361 aagctgaccc ccctgtgcgt gaccctgaaac tgcaccgaca ccaacgtgac cggcaaccgc  
421 accgtgaccc gcaacagcac caacaacacc aacggcaccg gcatctacaa catcgaggag  
481 atgaagaact gcagctcaa cgccaccacc gagctgcgcg acaagaagca caaggagttac  
541 gccctgttct accgcctgga catcgccccc ctgaacgaga acagcgacaa cttcacctac  
601 cgcctgatca actgcaacac cagcaccatc acccaggccct gccccaaggt gagcttcgac  
661 cccatccccca tccactactg cgccccccgc ggctacgcca tccctgaagtg caacaacaag  
721 accttcaacg gcaccggccc ctgctacaac gtgagcaccg tgcagtgcac ccacggcatc  
781 aagccctgtgg tgagcaccca gtcgtctgt aacggcagcc tggccgagga gggcatcatc  
841 atccgcagcg agaacctgac cgagaacaccc aagaccatca tcgtgcaccc gaacgagac  
901 gtggagatca actgcacccg ccccaacaac aacacccgca agagcgtgcg catggcccc  
961 ggccaggccct tctacgcccac caacgacgtg atcggcaaca tccggcaggc ccactgcaac  
1021 atcagcaccg accgctggaa caagaccctg cagcaggtga tgaagaagct gggcgagcac  
1081 ttcccccaaca agaccatcca gttcaagccc cacggccggc gcgacccctgaa gatcaccatg  
1141 cacagcttca actgcccgg cgagttttc tactgcaaca ccagcaaccc gtcaacagc  
1201 accttaccaca gcaacaacgg cacccatcaag tacaacggca acagcagcag ccccatcacc  
1261 ctgcagtgcata agatcaagca gatcgatgcgc atgtggcagg gcgtggccca ggccaccc  
1321 gccccccccca tcggccgca catcacctgc cgcagcaaca tcaccggcat cctgctgacc  
1381 cgcgacggcg gcttcaacac caccaacaac accgagacct tccggccccc cggcgccgac  
1441 atgcgcgaca actggcgac cgagctgtac aagtacaagg tggtgagat caagccctg  
1501 ggcacccccc ccaccaaggc caagcgccgc gtggcgcgc gcgagaagcg cgccgtggc  
1561 atcggcgcccg tttccctggg cttccctggc gcccggca gcaccatgg cgccgcgc  
1621 atcaccctga ccgtgcaggc cccgcaggctg ctgagcggca tcgtgcagca gcagagcaac  
1681 ctgctgaagg ccatcgaggc ccagcagcac atgctgcagc tgaccgtgt gggcatcaag  
1741 cagctgcagg cccgcgtgtc ggccatcgag cgctaccctg aggaccagca gctgctggc  
1801 atctggggct gcagcgcccg cctgatctgc accaccggc tgccctggaa cagcagctgg  
1861 agcaacaaga gcgagaagga catctggac aacatgaccc ggtatgcgtg ggaccgcgag  
1921 atcagcaact acaccggccct gatctacaac ctgctggagg acagccagaa ccagcaggag  
1981 aagaacgaga aggacctgct ggagctggac aagtggaaaca acctgtggaa ctggttcgac  
2041 atcagcaact ggccctggta catctaactc gag

FIGURE 101

gp140mod.TV1.wtLnative (SEQ ID NO:133)

1 gaattcatga gagtgatggg gacacagaag aattgtcaac aatggtgat atggggcatc  
61 ttaggcitct gtagtcaat gatttgtaac accgaggacc tgtgggtgac cgtgtactac  
121 ggcgtgccccg tgtggcgca cgccaaagacc accctgttct ggcgcagcga cgccaaaggcc  
181 tacgagaccg aggtgcacaa cgtgtggcc acccacgcct gcgtgcccac cgaccccaac  
241 ccccaggaga tcgtgctgg caacgtgacc gagaacttca acatgtggaa gaacgacatg  
301 gccgaccaga tgacgagga cgtgatcgc ctgtggacc agagcctgaa gccctgcgtg  
361 aagctgaccc ccctgtgcgt gaccctgaa acgacccgaca ccaacgtgac cggcaaccgc  
421 accgtgaccg gcaacagcac caacaacacc aacggcaccg gcatctacaa catcgaggag  
481 atgaagaact gcagctcaa cgccaccacc gagctgcgcg acaagaagca caaggagtag  
541 gccctgttct accgcctgga catcggtccc ctgaacgaga acagcgacaa cttcacctac  
601 cgcctgatca actgcaacac cagcaccatc acccaggcct gccccaaagggt gagcttcgac  
661 cccatccccca tccactactg cgccccccgc ggctacgcca tcttgaagtg caacaacaag  
721 accttcaacg gcacccggccc ctgctacaac gtgagcaccg tgcatgcac ccacggcatc  
781 aagccctgtgg tgagcaccca gctgctgtg aacggcagcc tggccgagga gggcatcata  
841 atccgcagcg agaacctgac cgagaacacc aagaccatca tctgtgcaccc gaacgagagc  
901 gtggagatca actgcacccg ccccaacaac aacacccgca agagcgtgac catggcccc  
961 gcccaggcct tctacgccac caacgacgtg atcggcaaca tccgcccaggc ccactgcaac  
1021 atcagcaccg accgctggaa caagaccctg cagcagggtga tgaagaagct gggcgagcac  
1081 ttcccccaaca agaccatcca gttcaagccc cacccggcg ggcacctgga gatcaccatg  
1141 cacagcttca actgcgcgg cgagttttc tactgcaaca ccagcaaccc gttcaacagc  
1201 acctaccaca gcaacaacgg cacctacaag tacaacggca acagcagcag ccccatcacc  
1261 ctgcagtgca agatcaagca gatcggtgcgc atgtggcagg gcgtggccca gcccaccc  
1321 gccccccccca tgcggccaa catcacctgc cgcagcaaca tcaccggcat cctgtgacc  
1381 cgcgacggcg gcttcaacac caccaacaac accgagacct tccgccccgg cggcgccgac  
1441 atgcgcgaca actggcgacg cgagctgtac aagtacaagg tggtgagat caagccctg  
1501 ggcacccccc ccaccaaggc caagggccgc gtggcgcgc ggcgagaagcg cgccgtggc  
1561 atcggcgcccg ttttcttggg ctccctggc gcccggccca gcacccatggg cgccgccc  
1621 atcaccctga ccgtgcaggc ccgcacgtg ctgagcggca tctgtgcagca gcagagcaac  
1681 ctgctgaagg ccatcgaggc ccagcagcac atgctgcagc tgaccgtgt gggcatcaag  
1741 cagctgcagg cccgcgtgt ggcacatcgag cgcttacccatg aggaccagca gctgtggc  
1801 atctggggct gcagcggccg cctgatctgc accaccgcgc tgccctggaa cagcagctgg  
1861 agcaacaaga gcgagaagga catctggac aacatgaccc ggtatgcagtg ggaccgcgag  
1921 atcagcaact acaccggct gatctacaac ctgctggagg acagccagaa ccagcaggag  
1981 aagaacgaga aggacccgt gggatggac aagtggaaaca acctgtggaa ctggttcgac  
2041 atcagcaact ggcctggta catctaactc gag

FIGURE 102

NefD125G\_TV2\_C\_ZAopt (SEQ ID NO:134)

ATGGGC GGCAAGTGGAGCAAGAGCAGCATCATCGGCTGGCCCGAGGTGCGC  
GAGCGCATCCGCCGCACCGCAGCGCCGCCGAGGGCGTGGCAGCGCCAGC  
CAGGACCTGGAGAAGCACGGCGCCCTGACCACCAGCAACACCGCCCACAAC  
AACGCCGCCTGCGCCTGGCTGGAGGCCAGGAGGAGGAGGGCGAGGTGGC  
TTCCCCGTGCGCCCCCAGGTGCCCTGCGCCCCATGACCTACAAGGCCGCAT  
CGACCTGAGCTTCTCCTGAAGGAGAAGGGCGGCCTGGAGGGCCTGATCTAC  
AGCAAGAAGGCCAGGAGATCCTGGACCTGTGGGTGTACAACACCCAGGGC  
TTCTTCCCCGGCTGGCAGAACTACACCCCCGGCCCCGGCGTGCCTCCCCCT  
GACCTTCGGCTGGTACTTCAAGCTGGAGCCCCTGGACCCCCGCGAGGTGGAG  
GAGGCCAACGAGGGCGAGAACAACTGCCTGCTGCACCCATGAGCCAGCAC  
GGCATGGAGGACGAGGACCGCGAGGTGCTGCCTGGAAGTTCGACAGCACC  
CTGGCCCCGCCACATGGCCCGAGCTGCACCCGAGTACTACAAGGACT  
GCTGA

FIGURE 103

NefD125G-Myr\_TV2\_C\_ZAopt (SEQ ID NO:135)

ATGGCCGGCAAGTGGAGCAAGAGCAGCATCATCGGCTGGCCCGAGGTGCGC  
GAGCGCATCCGCCGCACCCGCAGCGCCCGAGGGCGTGGCAGCGCCAGC  
CAGGACCTGGAGAAGCACGGGCCCTGACCACCAGCAACACCGCCCACAAC  
AACGCCGCCTGCGCCTGGCTGGAGGCCAGGAGGAGGAGGGCGAGGTGGC  
TTCCCCGTGCGCCCCCAGGTGCCCTGCGCCCCATGACCTACAAGGCCGCAT  
CGACCTGAGCTTCTTCTGAAGGAGAAGGGCGGCCTGGAGGGCCTGATCTAC  
AGCAAGAAGGCCAGGAGATCCTGGACCTGTGGGTGTACAACACCCAGGGC  
TTCTTCCCCGGCTGGCAGAACTACACCCCCGGCCCCGGCGTGCCTCCCCCT  
GACCTTGGCTGGTACTTCAAGCTGGAGCCCCTGGACCCCCGCGAGGTGGAG  
GAGGCCAACGAGGGCGAGAACAACTGCCTGCTGCACCCATGAGCCAGCAC  
GGCATGGAGGACGAGGACCGCGAGGTGCTGCGCTGGAAGTTGACAGCACC  
CTGGCCCCGCCACATGGCCCGAGCTGCACCCGAGTACTACAAGGACT  
GCTGA

FIGURE 104

↓: is the regions for β-sheet deletions

\*: is the N-linked glycosylation sites for subtype C TV1 and TV2. Possible mutation (N→ Q) or deletions can be performed.

		1		50
SF162	(1)	----MDAMKRLCCVLLLCGAVFVSPSAVEKLWVIVYYGVPPWKEATTTL		
TV1.8_2	(1)	MRVMGTQKNCQQWWIWI GILGFWM L M I C N T E D L W V I V Y Y G V P V W R D A K T T L		
TV1.8_5	(1)	MRVMGTQKNCQQWWIWI GILGFWM L M I C N T E D L W V I V Y Y G V P V W R E A K T T L		
TV2.12-5/1	(1)	MRARGILKNYRHHWIWI GILGFWM L M M C N V K G L W V I V Y Y G V P V G R E A K T T L		
Consensus	(1)	MRVMGTQKNCQQWWIWI GILGFWM L M I C N V E D L W V I V Y Y G V P V W R E A K T T L		
		51	*	100
SF162	(47)	FCASDAKAYDTEVHNWATHACVPTDPNPOEIVLLENVTENFN MWKNNMVE		
TV1.8_2	(51)	FCASDAKAYE TEVHNWATHACVPTDPNPOEIVLGNVTENFN MWKNDMAD		
TV1.8_5	(51)	FCASDAKAYE TEVHNWATHACVPTDPNPOEIVLGNVTENFN MWKNNMAD		
TV2.12-5/1	(51)	FCASDAKAYE KEVHNWATHACVPTDPNPOEIVLGNVTENFN MWKNDMVD		
Consensus	(51)	FCASDAKAYE TEVHNWATHACVPTDPNPOEIVLGNVTENFN MWKNNMVD		
		101	*	150
SF162	(97)	QMHE DIIISLWDQSLKPCVKLTPLCVTLHCTNLKNATNTK-----SSN---		
TV1.8_2	(101)	QMHE DVIISLWDQSLKPCVKLTPLCVTLNCTDTNVTGNRTVTGNSTNNNG		
TV1.8_5	(101)	QMHE DIIISLWDQSLKPCVKLTPLCVTLNCTDTNVTGNRTVTGNNTDNIA		
TV2.12-5/1	(101)	QMOEDIISLWDQSLKPCVKLTPLCVTLNCTNATVNYN-----NTS---		
Consensus	(101)	QMHE DIIISLWDQSLKPCVKLTPLCVTLNCTNVTGNRTVTGNSNSN A		
		151	*	200
SF162	(139)	WKEMDRGEIKNCSEKVTTSIRNKMQKEYALFYKEDVVPIDN-----DNTSY		
TV1.8_2	(151)	TGIYNIEEMKNCSFNATTEL RD KKHKEYALFYR DIVPLN-- ENSDNFTY		
TV1.8_5	(151)	NATYKYEEMKNCSFNATTEL RD KKHKEYALFYR DIVPLN-- ENSNNFTY		
TV2.12-5/1	(141)	-----KDMKNC SFYVTTTEL RD KKKKENALFYR DIVPLNNRKNGNINNY		
Consensus	(151)	A Y EEMKNCSFNVTTTEL RD KKHKEYALFYR DIVPLNN ENSNNFTY		
		201	*	250
SF162	(185)	KLIN CNTS VITOACPKV S F E P I P I H Y C A P A G F A I L K C N D K F E N G S G P C T N		
TV1.8_2	(199)	R L I N C N T S T I T O A C P K V S F D P I P I H Y C A P A G Y A I L K C N N K T F E N G T G P C Y N		
TV1.8_5	(199)	R L I N C N T S T I T O A C P K V S F D P I P I H Y C A P A G Y A I L K C N N K T F E N G T G P C Y N		
TV2.12-5/1	(185)	R L I N C N T S A T T O A C P K V S F D P I P I H Y C A P A G Y A P L K C N N K F E N G I G P C D N		
Consensus	(201)	R L I N C N T S T I T Q A C P K V S F D P I P I H Y C A P A G Y A I L K C N N K T F E N G T G P C Y N		
		251	*	300
SF162	(235)	VSTVQCTH G I R P V V S T Q L L N G S L A E E G V V I R S E N F T D N A K T I I V O L K E S		
TV1.8_2	(249)	VSTVQCTH G I K P V V S T Q L L N G S L A E E G I I I R S E N L T E N T K T I I V H L N E S		
TV1.8_5	(249)	VSTVQCTH G I K P V V S T Q L L N G S L A E E G I I I R S E N L T E N T K T I I V H L N E S		
TV2.12-5/1	(235)	VSTVQCTH G I K P V V S T Q L L N G S L A E E E I I R S E N L T N N V K T I I V H L N E S		
Consensus	(251)	VSTVQCTH G I K P V V S T Q L L N G S L A E E G I I I R S E N L T E N T K T I I V H L N E S		
		301*	*	350
SF162	(285)	VEIN CTRPNNNTRK SIT TIGP G R A F Y A T G D I I G D I I R O A H C N I S G E K W N N T L		
TV1.8_2	(299)	VEIN CTRPNNNTRK S V R I G P G Q A F Y A T N D V I G N I R O A H C N I S T D R W N K T L		
TV1.8_5	(299)	VEIN CTRPNNNTRK S V R I G P G Q A F Y A T N D V I G N I R O A H C N I S T D R W N K T L		
TV2.12-5/1	(285)	IETK CTRP G N N T R K S V R I G P G Q A F Y A T G D I I G D I I R O A H C N I S K N E W N T L		
Consensus	(301)	VEIN CTRPNNNTRK S V R I G P G Q A F Y A T N D I I G N I R O A H C N I S T D R W N K T L		

FIGURE 105A

\* 351 \* \* 400

SF162	(335)	KQTVTKLQAQFGNKT-IVFKQSSGGDPEIVMHSFNCGBFYCNSTQLFN
TV1.8\_2	(349)	QQVMKKLGEHEFPNKT-IQFKPHAGGDILEITMHSHCRGEFFYCNTSNLFN
TV1.8\_5	(349)	QQVMKKLGEHEFPNKT-IKFEPHAGGDILEITMHSHCRGEFFYCNTSNLFN
TV2.12-5/1	(335)	QRVSQKLQELFPNSTGIKFAPHSGGDILEITTHSHNCGGEFFYCNNTDLFN
Consensus	(351)	QQVMKKLQEHEFPNKT IKFKPHAGGDILEITMHSHCRGEFFYCNTSNLFN
	401 \* \* ↓ β20/β21 ↓ 450	
SF162	(384)	STWNN-----TIGPN-NTNGTITIPCRIKOITINRQEVGKAMYAPPIAG
TV1.8\_2	(398)	STYHS---NNGTYKYNGNNSSPITLQCKIKQIIVRMWQGVGQATYAPPIAG
TV1.8\_5	(398)	STYYP---KNGTYKYNGNNSSPITLQCKIKQIIVRMWQGVGQAMYAPPIAG
TV2.12-5/1	(385)	STYSNGTCTNGTCMSN--NTERITLQCRIKOITINMWOEVGRAMYAPPIAG
Consensus	(401)	STYHN NGTYKYNGNS PITLQCKIKQIIVRMWQGVGQAMYAPPIAG
	\* 451 \* \* \* 500	
SF162	(427)	QIRCSSNITGILLTRDGGKEISNT--TEIFRPGGDMRDNWRSLEYKYKV
TV1.8\_2	(445)	NITCRSNITGILLTRDGGFNTNN--TETFRPGGDMRDNWRSLEYKYKV
TV1.8\_5	(445)	NITCRSNITGILLTRDGGFNTNNDEETFRPGGDMRDNWRSLEYKYKV
TV2.12-5/1	(433)	NITCRSNITGILLTRDGGDNNTET---ETFRPGGDMRDNWRSLEYKYKV
Consensus	(451)	NITCRSNITGILLTRDGGFNTNT TETFRPGGDMRDNWRSLEYKYKV
	501 550	
SF162	(475)	VKIEPLGVAPTKAKRRVVQREKRAVTLGAMFLGFLGAAGSTMGAASITLT
TV1.8\_2	(493)	VEIKPLGIAPTKAKRRVVQREKRAVGIGAVFLGFLGAAGSTMGAASITLT
TV1.8\_5	(495)	VEIKPLGIAPTKAKRRVVQREKRAVGIGAVFLGFLGAAGSTMGAASITLT
TV2.12-5/1	(480)	VEIKPLGVAPTAKRRVVVEREKRAGIGAVFLGFLGAAGSTMGAASITLT
Consensus	(501)	VEIKPLGIAPTKAKRRVVQREKRAVGIGAVFLGFLGAAGSTMGAASITLT
	551 600	
SF162	(525)	VQAROLLSGIVQQQNLRLAIEAQHMLQLTVWGIKQLOARVLAIERYLK
TV1.8\_2	(543)	VQAROLLSGIVQQQSNLKAIEAQHMLQLTVWGIKQLOARVLAIERYLK
TV1.8\_5	(545)	VQAROLLSGIVQQQSNLKAIEAQHMLQLTVWGIKQLOARVLAIERYLK
TV2.12-5/1	(530)	VQAROLLSGIVQQQSNLRLAIEAQHMLQLTVWGIKQLOARVLAIERYLK
Consensus	(551)	VQAROLLSGIVQQQSNLKAIEAQHMLQLTVWGIKQLOARVLAIERYLK
	\* 601 \* \* \* 650	
SF162	(575)	DQQLLGIWGCSGKLICTTAVPWNASWSNKSLDQIWNNTWMEWEREIDNY
TV1.8\_2	(593)	DQQLLGIWGCSGKLICTTAVPWNSWSNKEKDIWDNMTWMQWDREISNY
TV1.8\_5	(595)	DQQLLGIWGCSGKLICTTAVPWNSWSNKEADIWDNMTWMQWDREISNY
TV2.12-5/1	(580)	DQQLLGLWGGSGKLICTTWNLSWSNKTQSDIWDNMTWMQWDREISNY
Consensus	(601)	DQQLLGIWGCSGKLICTTAVPWNSWSNKEADIWDNMTWMQWDREISNY
	651 700	
SF162	(625)	TNTIYTLEESQNOQEKNQEELLELDKWAISLWNWFDISKWLWYIKIFIMI
TV1.8\_2	(643)	TGLIYNLLEDSONOQEKNKDLELDKWNNEWNWFDISNWPWYIKIFIMI
TV1.8\_5	(645)	TETIYRLLEDSONOQEKNKDLELDKWNNLWNWFDISNWLWYIKIFIMI
TV2.12-5/1	(630)	TNTIYRLLEDSONOQEKNKDLELDKWNNLWNWFDISNWLWYIKIFIMI
Consensus	(651)	TNTIYRLLEDSONOQEKNKDLELDKWNNLWNWFDISNWLWYIKIFIMI
	701 750	
SF162	(675)	VGGIVGLRIVFTVLSIVNVRVRQGYSPLSFOTRFPAPRGDRPEGIEEEGG
TV1.8\_2	(693)	VGGIIGLRIIFAVLSIVNVRVRQGYSPLSFOTLTPSPRGDRRLGGIEEEGG
TV1.8\_5	(695)	VGGIIGLRIIFAVLSIVNVRVRQGYSPLSFOTLTPSPRGDRRLGGIEEEGG
TV2.12-5/1	(680)	VGGIIGLRIIFAVLSIVNVRVRQGYSPLSIOTLIPNPRGPDRRLGGIEEEGG
Consensus	(701)	VGGIIGLRIIFAVLSIVNVRVRQGYSPLSFOTLTPSPRGDRRLGGIEEEGG

FIGURE 105B

		751		
SF162	(725)	ERDRDRSSPLVHGLLAIWDDLRSICLFSYHRLRDLILIAARIVELLGR-		800
TV1.8_2	(743)	EQDRDRSIRLVSGFLSLAWDDLRLNLCILFSYHRLRDFILIAVRAVELLGH		
TV1.8_5	(745)	EQDRDRSIRIVSGFLSLAWDDLRSICLFSYHRLRDFILIAVRAVELLGH		
TV2.12-5/1	(730)	EQDSSRSIRLVSGFLTIWDDLRSICLFCYHRLRDFILIVVRAVELLGH		
Consensus	(751)	EQDRDRSIRLVSGFLSLAWDDLRLSCLFSYHRLRDFILIAVRAVELLGH		
		801		
SF162	(774)	-----RGWEALKYWGNNLLOYWIQEIKNSAVSLFDAIAIAVAEGTDRIIE		
TV1.8_2	(793)	SLRGLQRGWEILKYLGSIVQYWGLEYIKKSAISLLDTIATVAEGTDRIIE		
TV1.8_5	(795)	SLRGLQRGWEILKYLGSIVQYWGLEYIKKSAISPLDTIATVAEGTDRIIE		
TV2.12-5/1	(780)	SLRGLQRGWGTALKYLGSLIVQYWGLEYIKKSAISLLDTIATVAEGTDRIIE		
Consensus	(801)	SLRGLQRGWEILKYLGSIVQYWGLEYIKKSAISLLDTIATVAEGTDRIIE		
		851	876	
SF162	(818)	VAQRICRAFLHIPRRIRQGFERALL-		
TV1.8_2	(843)	LVQRICRAILNIPRRIRQGFEAALL-		
TV1.8_5	(845)	LVQRICRAILNIPRRIRQGFEAALL-		
TV2.12-5/1	(830)	FIONICRGIRNVPRRIROGFEAALQ-		
Consensus	(851)	LVQRICRAILNIPRRIRQGFEAALL		

FIGURE 105C